

**BLAST Basic Local Alignment Search Tool**Job Title: M18930:Human hepsin mRNA, complete cds

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•  
Please, try our new design!

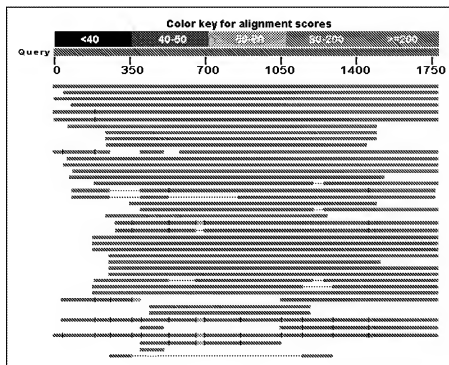
**BLASTN 2.2.18+**

RID: 36C7F3M2013 Database: All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,839,787 sequences; 23,768,953,950 total letters

Query= gi|184371|gb|M18930.1|HUMHPSNA Human hepsin mRNA, complete cds. Length=1783

**Distribution of 106 Blast Hits on the Query Sequence**

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Distance tree of results [NEW](#)

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer



## Sequences producing significant alignments:

(Click headers to sort columns)

NM_002151.1	Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 2, mRNA >gb[M18930.1]HUMHEP2A Human hepsin mRNA, complete cds	3293	3293	100%	0.0	100%	
BC025716.1	Homo sapiens hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:34588 IMAGE:5228525), complete cds	3199	3199	97%	0.0	99%	
XM_001093578.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA	3057	3057	99%	0.0	97%	
CR860913.1	Pongo abelii mRNA; cDNA DFFZp469A1831 (from clone DKFZp469A1831)	3000	3000	95%	0.0	98%	
NM_182983.1	Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 1, mRNA >emb[X07732.1]HSHEPCH Human hepatoma mRNA for serine protease hepsin	2842	3300	100%	0.0	100%	
XM_001093699.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA	2754	3063	99%	0.0	97%	
AK315655.1	Homo sapiens cDNA, FLJ956746	2645	2645	80%	0.0	100%	
DQ895314.2	Synthetic construct Homo sapiens clone IMAGE:100009774; FLN183201.OIL; RZPD083904139D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein	2309	2309	70%	0.0	99%	
DQ892119.2	Synthetic construct clone IMAGE:100004749; FLN183205.OIX; RZPD083904140D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein	2309	2309	70%	0.0	99%	
EU644753.1	Homo sapiens truncated hepsin serine protease mRNA, complete cds	2228	2228	67%	0.0	100%	
X07002.1	H.sapiens liver mRNA for serine protease hepsin	2215	2215	67%	0.0	100%	
AK233353.1	Sus scrofa mRNA, clone:LVRM10127D02, expressed in liver	2069	2069	96%	0.0	88%	
NM_001080241.2	Bos taurus hepsin (transmembrane protease, serine 1) (HPN), 1973, mRNA >gb[BC140635.1] Bos taurus hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:148484 IMAGE:8196479), complete cds	1973	1973	97%	0.0	87%	
BT029913.1	Bos taurus hepsin (transmembrane protease, serine 1) (HPN), 1956, mRNA, complete cds	1956	1956	94%	0.0	87%	
XM_541697.2	PREDICTED: Canis familiaris similar to Serine protease hepsin (Transmembrane protease, serine 1) (LOC484503), mRNA	1873	1873	81%	0.0	89%	
XM_001157575.1	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA	1868	2836	86%	0.0	99%	
CR597177.1	full-length cDNA clone CS0DJ003YL08 of T cells (Jurkat cell 1714 line) Cot 10-normalized of Homo sapiens (human)	2852	2852	86%	0.0	100%	
CR592189.1	full-length cDNA clone CS0DK012Y015 of Fetal liver of Homo sapiens (human)	1663	2235	68%	0.0	100%	
CU693029.1	Synthetic construct Homo sapiens gateway clone IMAGE:100019300 3' read HPN mRNA	1653	1653	64%	0.0	92%	
XM_001157514.1	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA	1476	2445	74%	0.0	99%	
CU693028.1	Synthetic construct Homo sapiens gateway clone IMAGE:100019300 5' read HPN mRNA	1465	1465	57%	0.0	92%	
AK095160.1	Homo sapiens cDNA FLJ37841.1, clone BRCN2012081, highly similar to SERINE PROTEASE HEP SIN (EC 3.4.21.-)	1404	2782	83%	0.0	100%	
XM_001093460.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA	1360	2552	81%	0.0	98%	
NM_008281.3	Mus musculus hepsin (Hpn), transcript variant 2, mRNA	1303	1303	89%	0.0	81%	
NM_017112.1	Rattus norvegicus hepsin (Hpn), mRNA >emb[X70900.1]RHHEPA R.norvegicus mRNA for hepsin	1297	1297	89%	0.0	81%	
AF030065.1	Mus musculus serine protease hepsin mRNA, complete cds	1280	1280	89%	0.0	81%	
NM_00110252.1	Mus musculus hepsin (Hpn), transcript variant 1, mRNA	1245	1245	85%	0.0	81%	
BC138809.1	Mus musculus hepsin, mRNA (cDNA clone MGC:170436 IMAGE:8861831), complete cds	1240	1240	70%	0.0	84%	
AK156553.1	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:PB30029112 product:hepsin, full insert sequence	1240	1240	85%	0.0	81%	
AK002694.1	Mus musculus adult male kidney cDNA, RIKEN full-length	1181	1181	85%	0.0	81%	

Accession	Description	Length	Score	E-value	Identity	Positives	Score	E-value	Identity	Positives
	enriched library, clone:0610030A17 product:hepsin, full insert sequence									
XM 512584.2	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 3 (HPH), mRNA	1011	2618	79%	0.0	100%				
BC072688.1	Rattus norvegicus hepsin, mRNA (cDNA clone MGC:91742 IMAGE:7098661), complete cds	935	1200	82%	0.0	84%				
AY234104.1	Mus musculus truncated hepsin splice variant mRNA, complete cds; alternatively spliced	880	1283	89%	0.0	82%				
XM 001254640.1	PREDICTED: Bos taurus similar to hepsin (LOC787164), partial mRNA	815	815	41%	0.0	86%				
BC119448.1	Mus musculus cDNA clone IMAGE:40044314	717	717	41%	0.0	84%				
BC119449.1	Mus musculus cDNA clone IMAGE:40044315	712	712	41%	0.0	84%				
AC192150.4	Pan troglodytes BAC clone CH251-522E19 from chromosome 19, complete sequence	590	3279	97%	9e-165	100%				
AK091988.1	Homo sapiens cDNA FLJ34669 fis, clone LIVER2001051	590	1367	41%	9e-165	100%				
AC020907.6	Homo sapiens chromosome 19 clone CTD-2527121, complete sequence	590	3376	100%	9e-165	100%				
AK125670.1	Homo sapiens cDNA FLJ34682 fis, clone TBAS2001258, weakly similar to SERINE PROTEASE HEPHIN (EC 3.4.21.-)	353	1228	36%	1e-93	100%				
DQ677665.1	Homo sapiens sodium channel beta-1 subunit precursor (SCN1B) gene, complete cds	289	509	14%	4e-74	100%				
AC197610.3	MACACA MULATTA BAC clone CH250-348G8 from chromosome 19, complete sequence	250	637	20%	2e-62	98%				
XM 001719305.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%				
XM 001721961.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%				
XM 001719287.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%				
AC158993.2	Mus musculus BAC clone RP24-427H13 from chromosome 7, complete sequence	141	260	13%	1e-29	87%				

## Alignments

>ref|NM\_002151.1|  Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 2, mRNA  
 gb|M18930.1|HUMHPSNA  Human hepsin mRNA, complete cds  
 Length=1783

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
 (Over 10 PubMed links)


Score = 3293 bits (1783), Expect = 0.0  
 Identities = 1783/1783 (100%), Gaps = 0/1783 (0%)  
 Strand=Plus/Plus

Query	1	TCGAGCCCGCTTTCCAGGGAACCTTACCTGAGGGCCACAGGTGAAGGACGCTGGCTAGC	60
Sbjct	1	TCGAGCCCGCTTTCCAGGGAACCTTACCTGAGGGCCACAGGTGAAGGACGCTGGCTAGC	60
Query	61	AGGCCCCACGCCACCGCTCTGCTCCAGGCGCCGCTGTGTCGCGGACACCATGTCTCC	120
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Sbjct	841	TGACAGCGCGCCATGCTCTCCGAGGCGGGAACCGGCTCTGTCGAGTGGCGAGTGTGTG	900
Query	901	CCGGTACCGTGGCCAGGCGCTCTCCCAACGCTTCCAGCTGGGGGTGACAGCTGTGTCT	960
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Sbjct 1141 |||||TACTATGCGCAACAGGCGCGGGTACTCCAGAGGCTCGAGTCCCCAATATCAGCA 1200
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>gb|BC025716.1|  Homo sapiens hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:34588 IMAGE:5228525), complete cds  
Length=1761

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
(Over 10 PubMed links)

Score = 3199 bits (1732), Expect = 0.0  
Identities = 1734/1735 (99%), Gaps = 0/1735 (0%)  
Strand=Plus/Plus

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Query 49 GCCTGGCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCGCTGCTCGGGG 108
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>ref|XM\_001093578.1|  PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 2 (HFN), mRNA  
Length=1785

GENE ID: 707242 HFN | hepsin (transmembrane protease, serine 1)  
[Macaca mulatta]

Score = 3057 bits (1655), Expect = 0.0  
Identities = 1739/1781 (97%), Gaps = 0/1781 (0%)  
Strand=Plus/Plus

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Query 603 GTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAAGTCACTCCGTTGTGTGAT 662  
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Query 723 GTGGACCGCACTGTTGGGAGGCGGGGACACAGCTTGGGCGCGGTGGCCGTGGCAAGTCAAGC 782  
 Sbjct 723 GTGGACCGCACTGTTGGGAGGCGGGGACACAGCTTGGGCGCGGTGGCCGTGGCAAGTCAAGC 782

Query 783 CTTGCTATGATGGAGCAACCTCTCTGCGGGGATCCCTGCTCTCCCGGAGCTGGGCTGCTG 842  
 Sbjct 783 CTTGCTATGATGGAGCAACCTCTCTGCGGGGATCCCTGCTCTCCCGGAGCTGGGCTGCTG 842

Query 843 ACAGCCGCCCACTGCTTTCCCGAGCGGAAACGGGGCTCTGTCGGAAGGCGAGTGTGTTGCC 902  
 Sbjct 843 ACAGCTGCCCACTGCTTTCCCGAGCGGAAACGGGGCTCTGTCGGAAGGCGAGTGTGTTGCC 902

Query 903 GGTGCGGTGGCCCAAGGCTCTCCCCAGGCTTCAGCTTGGGGGTGCAAGCTGTGGTCTAC 962  
 Sbjct 903 GGTGCGGTGGCCCAAGGCTCTCCCCAGGCTTCAGCTTGGGGGTGCAAGCTGTGGTCTAC 962

Query 963 CACGGGGGCTATCTTCCCTTTGCGGACCCCAACAGCGAGGAGAAACAGCAATGATATGGC 1022  
 Sbjct 963 CACGGGGGCTATCTTCCCTTTGCGGACCCCAACAGCGAGGAGAAACAGCAATGATATGGC 1022

Query 1023 CTGGTCCACCTCTCCAGTCCCTGCGCCCTCACAAGATACATCCAGGCTGTGTGCTCCCA 1082  
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Query 1083 GCTCCGCGCAGGCGCTGGTGGATGGCAAGATCTGTACGTTGACGGGCTGGGGCAACACG 1142  
 Sbjct 1083 GCTGCTGCGCAGGCGCTGGTGGATGGCAAGATCTGTACGTTGACGGGCTGGGGCAACACG 1142

Query 1143 CAGTACTATGGCCAAAGGCGGGGATCTCCAGGAGGCTCGAGTCCCCATAATCAGCAAT 1202  
 Sbjct 1143 CAGTACTATGGCCAAAGGCGGGGATCTCCAGGAGGCTCGAGTCCCCATAATCAGCAAT 1202

Query 1203 GATGTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCAGCAAGTTCTGTGCT 1262  
 Sbjct 1203 GATGTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCAGCAAGTTCTGTGCT 1262

Query 1263 GGGTACCCCGAGGGTGGCATTTGCTGCTGCGAGGCGCAGCGGGTGGTCCCTTGTGTGT 1322  
 Sbjct 1263 GGGTACCCCGAGGGTGGCATTTGCTGCTGCGAGGCGCAGCGGGTGGTCCCTTGTGTGT 1322

Query 1323 GAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTTGAGATTGGGGCACT 1382  
 Sbjct 1323 GAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTTGAGATTGGGGCACT 1382

Query 1383 GAGCTGTGCGCTTGCCCCAGGAAGCAGCGGCTCTACACCAAGGTCAAGTGACTTCGCGAGGTGG 1442  
 Sbjct 1383 GAGCTGTGCGCTTGCCCCAGGAAGCAGCGGCTCTACACCAAGGTCAAGTGACTTCGCGAGGTGG 1442

Query 1443 ATCTTCCAGGCCATAAAGACTCACTCCGAAGCCACGCGCATGGTGACCCAGCTCTGACCG 1502  
 Sbjct 1443 ATCTTCCAGGCCATAAAGACTCACTCCGAAGCCACGCGCATGGTGACCCAGCTCTGACCG 1502

Query 1503 GTGGCTTCTGCTGCGCAGCGCTCCAGGGCCGAGGATGATCCGCTGGTGGATCCAGCT 1562  
 Sbjct 1503 GTGGCTTCTGCTGCGCAGCGCTCCAGGGCCGAGGATGATCTGGGTGGTGGATCCAGCT 1562

Query 1563 GGGCCGAGGATGGGACGTATTTCTCTTGGGCCGCGTCCACAGGTTCCAGGAACACCTTCC 1622  
 Sbjct 1563 GGGCCTAGGATGGGACATTTTCTCTTGGGCCGCGTCCACAGGTTCCAGGAACACCTTCC 1622

Query 1623 CTCACGGGTCTCTCTTCCACAGTGGCGGCCACTCAGCCCGGAGACCAACCACTCA 1682

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Sbjct 1623      |TTCCAGGGTCTTCTCTCCACAGTGGCGGGCCCACTCAGCCCGGAGACACCCAGCTCA 1682
Query 1683      |CCCTCCCTGACCCCCCATGTAAATATTTGTTCTGCTGCTGGAGCTCCCTGTCTAGGTGCCCC 1742
Sbjct 1683      |CCCTCCCTGACCCCCCATGTAAATATTTGTTCTGCTGCTGGAGCTCCCTGTCTAGGTGCCCC 1742
Query 1743      |GATGATGGGATGCTCTTTAAATAATAAGATGGTTTGGATT 1783
Sbjct 1743      |GATGACCGGATGCTCTTTAAATAATAAGATGGTTTGGATT 1783

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Length=1741

Score = 3000 bits (1624), Expect = 0.0
Identities = 1676/1702 (98%), Gaps = 0/1702 (0%)
Strand=Plus/Plus

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Sbjct 18        |GCCTCCAGGCGCGCCCGCTGCTGCGGGGCCACCATGCTCTGCCCAAGCTCGAGACTGAC 77
Query 142       |CCGACCCCGGCACTACCTCGAGGGCTCGCGCCCCCACTGCTGGACCCCAAGGTCACCACT 201
Sbjct 78        |CGACCCCGGCACTACCTCGAGGGCTCGCGCCCCCACTGCTGGACCCCAAGGTCACCACT 137
Query 202       |GGCCCAAGAGGTCAGCCAGGATCATTTAAACAAGAGGCACTGACATGCGCAGAGAGAGG 261
Sbjct 202       |GGCCCAAGAGGTCAGCCAGGATCATTTAAACAAGAGGCACTGACATGCGCAGAGAGAGG 197
Query 292       |GTGGCCGGAATGTGCGCATGCTGCTCCAGAACCCAGGTGGCAGCTCTCACTGCGGGAGCCC 321
Sbjct 196       |GTGGCCGGAATGTGCGCATGCTGCTCCAGAACCCAGGTGGCAGCTCTCACTGCGGGAGCCC 257
Query 322       |TGCTACTTCTGACAGCCATCGGGCGGCACTCCGCGGCATTGTGTGCTGTTCTCTCAGGA 381
Sbjct 258       |TGCTACTTCTGACAGCCATCGGGCGGCACTCCGCGGCATTGTGTGCTGTTCTCTCAGGA 317
Query 382       |GTGACCAAGAGCGCGCTGTATCCAGGTGCAGCTGCGGACGCTCGGCTCATGTGCT 441
Sbjct 318       |GTGACCAAGAGCGCGCTGTATCCAGGTGCAGCTGCGGACGCTCGGCTCATGTGCT 377
Query 442       |TTGACAAGACCGAAGAGGACGTTGGCGGCTGCTGTGCTCTCTCGCGCTCCAAAGCAGGGTAG 501
Sbjct 378       |TTGACAAGACCGAAGAGGACGTTGGCGGCTGCTGTGCTCTCTCGCGCTCCAAAGCAGGGTAG 437
Query 502       |CGGACCTCAGCTCGAGAGGAGTGGGCTTCTCAGGGCACTGACCCACTCCGAGCTGGAGC 561
Sbjct 438       |CGGACCTCAGCTCGAGAGGAGTGGGCTTCTCAGGGCGTGACCCACTCCGAGCTGGAGC 497
Query 562       |TGCBAACGGCGGGCGCCATGCGACGTGCGGCTTCTTCTGTGTGGAAGAGGAGAGGCTGC 621
Sbjct 498       |TGCBAACGGCGGGCGCCATGCGACGTGCGGCTTCTTCTGTGTGGAAGAGGAGAGGCTGC 557
Query 622       |CCCCACCCAGAGGCTGCTGAGAGGTCACTCCGTGTGTGATTGCCCAAGAGCGCTTTCT 681
Sbjct 558       |CCCCACCCAGAGGCTGCTGAGAGGTCACTCCGTGTGTGATTGCCCAAGAGCGCTTTCT 617
Query 682       |TGGCCGCATCTGCCCCAAGACTGTGGCGCGCAGGAAGCTGCCGTGTGGAACCGCATGTGGAG 741
Sbjct 618       |TGGCCGCATCTGCCCCAAGACTGTGGCGCGCAGGAAGCTGCCGTGTGGAACCGCATGTGGAG 677
Query 742       |GCCCGGACACCGAGCTTGGGCGCGTGGCCGTGGCAAGCTCAGCTTCGCTATATGAGAGCAC 801
Sbjct 678       |GCCCGGACACCGAGCTTGGGCGCGTGGCCGTGGCAAGCTCAGCTTCGCTATATGAGAGCAC 737
Query 802       |ACCTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGTGACAGACCGCCCACTGCTTCC 861
Sbjct 738       |ACCTTTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGTGACAGACCGCCCACTGCTTCC 797
Query 862       |CGGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTTTGGCCGTTGCCGTGGCCAGGCT 921
Sbjct 798       |CAGAGCGGAACCGGGTCTGTCCCGATGGCGAGTGTTTGGCCGTTGCCGTGGCCAGGCT 857
Query 922       |CTCCCCAAGTCTGACGCTGGGGGTTGACGGCTGTGGTCTACCAACGGGGGCTATCTTCCCT 981
Sbjct 858       |CTCCCCAAGTCTGACGCTGGGGGTTGACGGCTGTGGTCTACCAACGGGGGCTATCTTCCCT 917
Query 982       |TTGGGACCCCAACAGCGAGAGGAGAACAGCAACGATATTGCCCTGTGCTCACTCTCCAGTC 1041
Sbjct 918       |TTGGGACCCCAACAGCGAGAGGAGAACAGCAACGATATTGCCCTGTGCTCACTCTCCAGTC 977
Query 1042      |CCCTGCCCCCTCACAAGATACTACCGCTGTGTGCTCCCAAGCTGCGGCGCAGGCCCTTGG 1101
Sbjct 978       |CCCTGCCCCCTCACAAGATACTACCGCTGTGTGCTCCCAAGCTGCGGCGCAGGCCCTTGG 1037
Query 1102      |TGATATGCAAGATCTGTACCGTGAAGGGCTGGGGCAACAGCAGTACTATGCGCAACAGG 1161
Sbjct 1038      |TGATATGCAAGATCTGTACCGTGAAGGGCTGGGGCAACAGCAGTACTATGCGCAACAGG 1097
Query 1162      |CCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTG 1221
Sbjct 1098      |CCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTG 1157
Query 1222      |ACTTCTATGGAACAACAGATCAAGCCCAAGATGTTCTGTGCTGACTACCCAGAGGTGCA 1281
Sbjct 1158      |ACTTCTATGGAACAACAGATCAAGCCCAAGATGTTCTGTGCTGACTACCCAGAGGTGCA 1217




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Query 1282 TTGATGCTGCGAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGA 1341
Sbjct 1218 TTGATGCTGCGAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGA 1277
Query 1342 CCCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCCTGGCTGTGCCCCGGCCAGA 1401
Sbjct 1278 CCCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCCTGGCTGTGCCCCGGCCAGA 1337
Query 1402 AGCCAGGCGTCTACACCAAAAGTCAATGACTTCCGGAGTGGAGTCTTCCAGGCGCATAAAGA 1461
Sbjct 1338 AGCCAGGCGTCTACACCAAAAGTCAATGACTTCCGGAGTGGAGTCTTCCAGGCGCATAAAGA 1397
Query 1462 CTCACTCGGAAGCCAGCGGCTAGTGAACCCAGCTCTGACCGGTGGCTTCTCTGCGCGCAG 1521
Sbjct 1398 CTCACTCGGAAGCCAGCGGCTAGTGAACCCAGCTCTGACCGGTGGCTTCTCTGCGCGCAG 1457
Query 1522 CTTCCAGGGCCGAGGTGATCCCGTGGTGGGATCCAGCTGGGCGGAGATGGAGCGTT 1581
Sbjct 1458 CTTCCAGGGCCGAGGTGATCTTGGTGGTGGGATCCATGCGAGGCTTAGAGTGGAGCGTT 1517
Query 1582 TTCTCTCTTGGGCGCGGTCCACAGGTCCAAAGGACACCCCTCCCTCCAGGTCCTCTCTTCC 1641
Sbjct 1518 TTCTCTCTTGGGCGCGGTCCACAGGTCCAAAGGACACCCCTCCCTCCAGGTCCTCTCTTCC 1577
Query 1642 ACAGTGGCGGGGCCACTCAGCCCCGAGCACCCCACTCAACCTCTGACCCGCCATGTA 1701
Sbjct 1578 ACAGTGGCGGGGCCACTCAGCCCCGAGCACCCCACTCAACCTCTGACCCGCCATGTA 1637
Query 1702 AATATTGTTCTGCTGTCTGGGACTCTCTGTCTAGGTGCCCTGATGATGGAGTGTCTCTTFA 1761
Sbjct 1638 AATATTGTTCTGCTGTCTGGGACTCTCTGTCTAGGTGCCCTGATGATGGAGTGTCTCTTFA 1697
Query 1762 AATAATAAAGATGGTTTGGATT 1783
Sbjct 1698 AATAATAAAGATGGTTTGGATT 1719

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>ref|NM\_182983.1|  Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 1, mRNA  
emb|X07732.1|  HSHEPFS  Human hepatoma mRNA for serine protease hepsin  
length=2363

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
(Over 10 PubMed links)

Sort alignments for this subject sequence by:  
E value Score Percent identity  
Query start position Subject start position

Score = 2942 bits (1593), Expect = 0.0  
Identities = 1593/1593 (100%), Gaps = 0/1593 (0%)  
Strand=Plus/Plus

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Query 191 GGTCCCAACCTTGGCCAGAGGATCAGCCAGGGAATCATTAACAAGAGCGAGTGAACATGGC 250
Sbjct 771 GGTCCCAACCTTGGCCAGAGGATCAGCCAGGGAATCATTAACAAGAGCGAGTGAACATGGC 830
Query 251 GCAGAGGAGAGGTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAAGTTGGCAGCTCTCAC 310
Sbjct 831 GCAGAGGAGAGGTGGCCGGAAGTGTGCCATGCTGCTCCAGACCCAAAGTTGGCAGCTCTCAC 890
Query 311 TGCGGGGACCTCTGCTACTCTGACAGCCATCGGGGCGGATCTCCGGCCATTGTGGTGTGT 370
Sbjct 891 TGCGGGGACCTCTGCTACTCTGACAGCCATCGGGGCGGATCTCCGGCCATTGTGGTGTGT 950
Query 371 TCTCTCTCAGGAGTGACCAAGAGCCCGTGTACCCAGTGACAGGTCAAGCTCTGCGGACGCTGG 430
Sbjct 951 TCTCTCTCAGGAGTGACCAAGAGCCCGTGTACCCAGTGACAGGTCAAGCTCTGCGGACGCTGG 1010
Query 431 GCTCATGTTCTTTGACAAGAGCAGAAAGGACGTTGGCGGCTGTGTGCTCTCTCGGCTCCAA 490
Sbjct 1011 GCTCATGTTCTTTGACAAGAGCAGAAAGGACGTTGGCGGCTGTGTGCTCTCTCGGCTCCAA 1070
Query 491 CGCCAGGGGTAGCCGAGCTCAGCTGCGAGGAGATGGGCTTCCCTCAAGGACATGACCCCATC 550
Sbjct 1071 CGCCAGGGGTAGCCGAGCTCAGCTGCGAGGAGATGGGCTTCCCTCAAGGACATGACCCCATC 1130
Query 551 CAGGCTGGACGTGCGAAACGCGCGGCGCCAAATGGCAGCTCGGGCTTCTTCTGTGTGGAGGA 610
Sbjct 1131 CAGGCTGGACGTGCGAAACGCGCGGCGCCAAATGGCAGCTCGGGCTTCTTCTGTGTGGAGGA 1190
Query 611 GGGGAGGCTGCCCCACAACCGAGGGCTGTGGAGGTCACTCCGTGTGTGATGTGCCCCAG 670
Sbjct 1191 GGGGAGGCTGCCCCACAACCGAGGGCTGTGGAGGTCACTCCGTGTGTGATGTGCCCCAG 1250
Query 671 AGGCCGTTTCTTGGCGCGCATCTGCCAAGACGTTGGCGCAGGAAGCTGCCCGTGGACCG 730
Sbjct 1251 AGGCCGTTTCTTGGCGCGCATCTGCCAAGACGTTGGCGCAGGAAGCTGCCCGTGGACCG 1310
Query 731 CATCGTGGAGAGCCGGAACACAGCTTGGGCCGCGTGGCCGTGGACAGTCAGCCTTCGCTA 790
Sbjct 1311 CATCGTGGAGAGCCGGAACACAGCTTGGGCCGCGTGGCCGTGGACAGTCAGCCTTCGCTA 1370
Query 791 TGATGGAGCAACCTCTGTGGGGATTCCTCTCTCCCGGAGCATGGGTCTGACAGCCGCG 850
Sbjct 1371 TGATGGAGCAACCTCTGTGGGGATTCCTCTCTCCCGGAGCATGGGTCTGACAGCCGCG 1430

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Query 851 CCACCTGCTTCCCGGAGCGGAAACCGGGTCTGTCCCGATGCGAGTGTGTTGCGGGTGCCGT 910
Sbjct 1431 CCACCTGCTTCCCGGAGCGGAAACCGGGTCTGTCCCGATGCGAGTGTGTTGCGGGTGCCGT 1490

Query 911 GGCCCAAGGCTCTCTCCCAACGGTCTGCAAGTGGGGGTGCAAGCTGTGGTCTACCAACGGGG 970
Sbjct 1491 GGCCCAAGGCTCTCTCCCAACGGTCTGCAAGTGGGGGTGCAAGCTGTGGTCTACCAACGGGG 1550

Query 971 CTATCTTCCCTTTCCGGGACCCCAACGAGAGGAGAACAGCAATATTCGCTGTGTCCA 1030
Sbjct 1551 CTATCTTCCCTTTCCGGGACCCCAACGAGAGGAGAACAGCAATATTCGCTGTGTCCA 1610

Query 1031 CCTCTCCAGTCCCCGTGCCCTTCACAGAAATACATCCAGCTGTGTGCTCCCAAGCTGCCGG 1090
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Query 1091 CCAGGCTCTGTGGATGGCAAGATCTGTACCGTGAACGGCTGGGGCAACAGCAGTACTA 1150
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Query 1151 TGGCCAAACAGGCCCGGGGTACTCCAGAGGGCTCGAGTCCCCATAATCAGCAATGATGTCTG 1210
Sbjct 1731 TGGCCAAACAGGCCCGGGGTACTCCAGAGGGCTCGAGTCCCCATAATCAGCAATGATGTCTG 1790

Query 1211 CAATGGCGCTGACTTCTATGGAAACAGATCAAGGCCAAGATGTTCTGTGTGATGCTATCC 1270
Sbjct 1791 CAATGGCGCTGACTTCTATGGAAACAGATCAAGGCCAAGATGTTCTGTGTGATGCTATCC 1850

Query 1271 CGAGGGTGGCATTTGATGCTGTGCGAGGCGACAGCGTGGTCCCCTTGTGTGTGAGGACAG 1330
Sbjct 1851 CGAGGGTGGCATTTGATGCTGTGCGAGGCGACAGCGTGGTCCCCTTGTGTGTGAGGACAG 1910

Query 1331 CATCTCTCGGACCCACGTTGGCGGCTGTGTGGCATTTGTGTTGGGGCACTGGCTGTGTC 1390
Sbjct 1911 CATCTCTCGGACCCACGTTGGCGGCTGTGTGGCATTTGTGTTGGGGCACTGGCTGTGTC 1970

Query 1391 CCTGGCCCAAGAGCCAGGCGCTCTACACCAAGTCAATGACTTCCGGAGTGTGATCTTCCA 1450
Sbjct 1971 CCTGGCCCAAGAGCCAGGCGCTCTACACCAAGTCAATGACTTCCGGAGTGTGATCTTCCA 2030

Query 1451 GACCATTAAGAGCTCATCCGAAAGCCAGGGCATGGTGAACCCAGCTCTGACCGGTGGCTTC 1510
Sbjct 2031 GACCATTAAGAGCTCATCCGAAAGCCAGGGCATGGTGAACCCAGCTCTGACCGGTGGCTTC 2090

Query 1511 TCGTGTGGCAGGCTCCAGGGCCCGAGGTGATCCCGTGGTGGGATCCAGCTGGGCGAG 1570
Sbjct 2091 TCGTGTGGCAGGCTCCAGGGCCCGAGGTGATCCCGTGGTGGGATCCAGCTGGGCGAG 2150

Query 1571 GATGGAGCTTTTCTCTCTTGGGCGCGGTCCACAGTCCAGGAGCAACCTCCCTCCAGGG 1630
Sbjct 2151 GATGGAGCTTTTCTCTCTTGGGCGCGGTCCACAGTCCAGGAGCAACCTCCCTCCAGGG 2210

Query 1631 TCTCTCTCTCCACAGTGGCGGGGCCACTCAGCCCGAGGACCAACCACTCAACCTCTCTG 1690
Sbjct 2211 TCTCTCTCTCCACAGTGGCGGGGCCACTCAGCCCGAGGACCAACCACTCAACCTCTCTG 2270

Query 1691 ACCCCCAATGTAATATTGTCTGTCTGTCTGGGACTCCCTGTCTAGTGTGCCCTGATGATGG 1750
Sbjct 2271 ACCCCCAATGTAATATTGTCTGTCTGTCTGGGACTCCCTGTCTAGTGTGCCCTGATGATGG 2330

Query 1751 GATGCTCTTTAAATAAATAAGATGGTTTGTATT 1783
Sbjct 2331 GATGCTCTTTAAATAAATAAGATGGTTTGTATT 2363

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Score = 357 bits (193), Expect = 1e-94  
 Identities = 193/193 (100%), Gaps = 0/193 (0%)  
 Strand=Plus/Plus

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Query 1 TCGAGCCCGCTTTCCAGGACCCCTACCTGAGGGGCCACAGGTGAGGACGCTGGCTATGC 60
Sbjct 1 TCGAGCCCGCTTTCCAGGACCCCTACCTGAGGGGCCACAGGTGAGGACGCTGGCTATGC 60

Query 61 AGGCCCAACGACACCGGCTCTGCTCTCCAGGCGCCCGCTGCTGCGGGGACCAATGCTCC 120
Sbjct 61 AGGCCCAACGACACCGGCTCTGCTCTCCAGGCGCCCGCTGCTGCGGGGACCAATGCTCC 120

Query 121 TGCCCAAGGCTTGGAGACTGACCCGAGCCCGGCACTACCTCGAGGCTCCGCCCCCACTGC 180
Sbjct 121 TGCCCAAGGCTTGGAGACTGACCCGAGCCCGGCACTACCTCGAGGCTCCGCCCCCACTGC 180

Query 181 TGGACCCCAAGGTT 193
Sbjct 181 TGGACCCCAAGGTT 193

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>ref|XM\_001093699.1|  PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 3 (HFN), mRNA  
 Length=2363

GENE ID: 707242 HFN | hepsin (transmembrane protease, serine 1)  
 [Macaca mulatta]

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 2754 bits (1491), Expect = 0.0  
 Identities = 1559/1593 (97%), Gaps = 0/1593 (0%)  
 Strand=Plus/Plus

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Sbjct   769   GGTCCCAACCCCTGGCCCAAGGAGGTGACGCCAGGGAATCATTAACAAGAGGCGAGTGACATGGC 828

Query   251   GCAGAAAGAGGGGTGGCCCGGACTGTGTCCATGCTGCTCCAGACCCAAAGGTGGCGAGCTCTCAC 310
Sbjct   889   GCAGAAAGAGGGGTGGCCCGGACTGTGTCCATGCTGCTCCAGACCCAAAGGTGGCGAGCTCTCAC 888

Query   311   TGCAGGGAACCTGCTACTCTTCAGACAGCCATCGGGGCGGACCTCTGGGCGATTGTGGCTGT 370
Sbjct   889   TGCAGGGAACCTGCTACTCTTCAGACAGCCATCGGGGCGGACCTCTGGGCGATTGTGGCTGT 948

Query   371   TCTCTCTCAGGAGTGACCAAGAGCCCGCTGTACCCAGTGACAGGTCAAGCTCTGGCGAGCGCTGG 430
Sbjct   949   TCTCTCTCAGGAGTGACCAAGAGCCCGCTGTACCCAGTGACAGGTCAAGCTCTGGCGAGCGCTGG 1008

Query   431   GCTCATGGTCTTTGACCAAGACGGAAGGACGTGGCGGCTGTGTGTGCTCTCCGCGCTCCAA 490
Sbjct   1009   GCTCATGGTCTTTGACCAAGACGGAAGGACGTGGCGGCTGTGTGTGCTCTCCGCGCTCCAA 1068

Query   491   CCGCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAGGGCACTGACCCACTC 550
Sbjct   1069   CACCAAGGATAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAGGGCACTGACCCACTC 1128

Query   551   CGAGCTGGACGTGCGAAACGGCGGGCGCCAAATGGCAAGTGGGCTTCTTCTGTGTGGAGCGA 610
Sbjct   1129   CGAGTGTGACGTGCGAAACGGCGGGCGCCAAACGGCAAGTGGGCTTCTTCTGTGTGGAGTGA 1188

Query   611   GGGAGGGCTGCCCAACAACCAAGAGGCTGCTGGAGGTCACTCCGTGTGTGATATGCCCCAG 670
Sbjct   1189   GGGAGGGCTGCCCAACAACCAAGAGGCTGCTGGAGGTCACTCCGTGTGTGATATGTCCCAAG 1248

Query   671   AAGCCGTTTCTTGGCCCGCATCTGCCAAGACTGTGGCCGACAGGAAGCTGCCCGTGGACCG 730
Sbjct   1249   AAGCCGTTTCTTGGCCCGCATCTGCCAAGACTGTGGCCGACAGGAAGCTGCCCGTGGACCG 1308

Query   731   CATCGTGGAGGCCCGGGACACCAAGCTTGGGCGCGGTGGCCCGTGGCAAGTCAAGCTCCGTA 790
Sbjct   1309   CATCGTGGAGGCCCGGGACACCAAGCTTGGGCGCGGTGGCCCGTGGCAAGTCAAGCTCCGTA 1368

Query   791   TGATGGAGCAACCTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGGGTGCTGACAGCCGC 850
Sbjct   1369   TGATGGAGCAACCTCTGCGGGGGTCCCTGCTCTCCGGGAGCTGGGTGCTGACAGCTGC 1428

Query   851   CCACTGCTTCCCGAGACGGAACCGGGTCTGTGCCGATGGCGAGTGTGTGCGCGTGCCT 910
Sbjct   1429   CCACTGCTTCCCGAGACGGAACCGGGTCTGTGCCGATGGCGAGTGTGTGCGCGTGCCT 1488

Query   911   GGGCCAGGCTCTCCCCACCGTCTGCGAGCTGGGGGTGAGGCTGTGGTCTACACAGCGGG 970
Sbjct   1489   GGGCCAGGCTCTCCCCACCGCTGCGAGCTGGGGGTGAGGCTGTGGTCTACACAGCGGG 1548

Query   971   CTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAATGATATGCGCTGGTCCA 1030
Sbjct   1549   CTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAATGATATGCGCTGGTCCA 1608

Query   1031   CCTCTCCAGTCCCTGCCCCCTCAGCAAGATACATCCAGCCTGTGTGCTCCAGCTGGCCGG 1090
Sbjct   1609   CCTCTCCAGTCCCTGCCCCCTCAGCAAGATACATCCAGCCTGTGTGCTCCAGCTGGCTGG 1668

Query   1091   CCAAGGCCCTGTGGATGGCAAGATCTGTATCCGTGACGGGCTGGGGCAACACAGCATACTA 1150
Sbjct   1669   CCAAGGCCCTGTGTGGATGGCAAGATCTGTATCCGTGACGGGCTGGGGCAACACAGCATACTA 1728

Query   1151   TGGCCCAACAGGCCCGGGTACTCCAGAGGCTCGAGTCCCCCAATACAGCAATGATGTCTG 1210
Sbjct   1729   TGGCCCAACAGGCCCGGGTACTCCAGAGGCTCGAGTCCCCCAATACAGCAATGATGTCTG 1788

Query   1211   CAATGGCGTGACTTCTATGGAJACAGATCAAGGCCCAAGATGTTCTGTGCTGGCTACCC 1270
Sbjct   1789   CAATGGCGTGACTTCTATGGAJACAGATCAAGGCCCAAGATGTTCTGTGCTGGCTACCC 1848

Query   1271   CGAGGGTGGCAATTGATGCTGCTGACAGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAG 1330
Sbjct   1849   CGAGGGTGGCAATTGATGCTGCTGACAGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAG 1908

Query   1331   CATCTCTCGAGACGCAAGTTTGGCGGCTGTGTGGCACTTGAGTGTGGGGGCACTGGCTGGC 1390
Sbjct   1909   CATCTCTCGAGACGCAAGTTTGGCGGCTGTGTGGCACTTGAGTGTGGGGGCACTGGCTGGC 1968

Query   1391   CTTGGCCCAAGAACCAAGCGCTCTACACCAAAAGTCAGTGACTTCCGGGAGTGGATCTTCCA 1450
Sbjct   1969   CTTGGCCCAAGAACCAAGCGCTCTACACCAAAAGTCAGTGACTTCCGGGAGTGGATCTTCCA 2028

Query   1451   GGCCATAAAGACTCACTCCGAAGCCAGGGGATGGTGACCCAGCTCTGACCGGTGGCTTTC 1510
Sbjct   2029   GGCCATAAAGACTCACTCCGAAGCCAGGGGATGGTGACCCAGCTCTGACCGGTGGCTTTC 2088

Query   1511   TCGCTGCGCAGCTTCCAGGGCCGAGGGTGTATCCCGTGGTGGGATCCACGCTGGGCCAG 1570
Sbjct   2089   TCGCTGCGCAGCTTCCAGGGCCGAGGGTGTATCCCGTGGTGGGATCCACGCTGGGCCAG 2148

Query   1571   GATGGGACGTTTTTCTTCTTGGGCGCGGTGCCAAGGTCCAAAGGACACCCCTCCACAGGG 1630

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Sbjct 2149 GATGGGACATTTTCTCTTGGGCCGGTCCACAGGTCCAAAGACACCCCTCCCTCCAGGG 2208
Query 1631 TCCTCTCTCCCAAGTGGAGCGGGCCACTCAGCCCGGAGACACCCCACTCACCCTCTG 1690
Sbjct 2209 TCCCTTCTTCCACAGTGGCCGGGCCACTCAGCCCGGAGACACCCGACCTCACCCTCTG 2268
Query 1691 ACCCCCAAGTAAATATTGTCTGTCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGG 1750
Sbjct 2269 ACCCCCGTGTAAATATTGTCTGTCTGTCTGGGACTCCTCTCTAGGTGCCCTGATGATGG 2328
Query 1751 GATGCTCTTTAAATAATAAGATGGTTTGGATT 1783
Sbjct 2329 GATGCTCTTTAAATAATAAGATGGTTTGGATT 2361

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 Identities = 183/191 (95%), Gaps = 0/191 (0%)  
 Strand=Plus/Plus

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Sbjct 3 GAGCCCGCTTTCCAGGGAACCTTACCCGGGGCCCAAGGTGAGGCGCCTGGCCTAGCAG 62
Query 63 GCGCCACGCGCAACCGCTCTGCTTCCAGGCGCCCGGCTGCTGCGGGGCCACCATGCTCTGG 122
Sbjct 63 GCGCCACGCGCAACCGCTTCTGCTTCCAGGCGCCCGGCTGCTGCGGGGCCACCATGCTCTGG 122
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>dbj|AK315655.1| Homo sapiens cDNA, FLJ96746  
 Length=1432

Score = 2645 bits (1432), Expect = 0.0  
 Identities = 1432/1432 (100%), Gaps = 0/1432 (0%)  
 Strand=Plus/Plus

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Sbjct 1 ACGCCACCGCTCTGCTCTCCAGGCGCGCCGCTGCTGCGGGCCACCACTGCTCTGCCAG 60
Query 128 GCCTGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCCCCACTGCTGAGACC 187
Sbjct 61 GCCTGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCCCCACTGCTGAGACC 120
Query 188 CAGGGTCCCACTCGGCGCCAGAGGGTCAAGCAGGGAACTATTAAAGAGGCAATGACAT 247
Sbjct 121 CAGGGTCCCACTCGGCGCCAGAGGGTCAAGCAGGGAACTATTAAAGAGGCAATGACAT 180
Query 248 GCGCGAGAGGAGGGGTGCGCGGACTGTGCTCATGCTGCTCCAGCCAGAGGTTGACAGCTCT 307
Sbjct 181 GCGCGAGAGGAGGGGTGCGCGGACTGTGCTCATGCTGCTCCAGCCAGAGGTTGACAGCTCT 240
Query 308 CACTGCGGGGACCTGCTACTTCTTGACAGCCATCGGGCGGCACTCTGCGGCATTGTGGC 367
Sbjct 241 CACTGCGGGGACCTGCTACTTCTTGACAGCCATCGGGCGGCACTCTGCGGCATTGTGGC 300
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Sbjct 301 TGTTCTCTCAGAGGTGACAGGAGGCGCTGTGACCAAGTGCAGGTGAGCTCGGAGGCG 360
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Sbjct 361 TCGGCTCATGCTCTTTGACAGAGCGAGAGGAGCTGGCGGCTGCTGTGCTCTCGCGCTC 420
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Sbjct 481 CTCGAGCTGGAAGTGCAGACCGCGGGCGCCATGACAGCTCGGGCTTCTTCTGTGTGGA 540
Query 608 CAGAGGGAGGGCTGCGCCCAACCCAGAGGCTGTGGAGGTCACTCTCGTGTGTGATGCCC 660
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Query 668 CAGAGGCGCTTTCTTGGCCGCACTTGCCAGAGCTGTGGCCGCAAGAGCTGCCCGTGA 727
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Query 728 CCGCATCGTGGAGGCGCGGACACCAAGCTTGGGCGGTGGCTGGCGAAGTCAAGCTTGG 787
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Query 848 CCGCCACTGCTTCCCGAGAGCGAACCAGGCTCTGCTGCCAGATGGCAGGTGTTTGGCGGTG 907

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Sbjct 781 |CCCCCATGCTCTCCCGGAGCGGAAACCGGGTCTCTGTCCTCCGATGGCGAGTGTTTTCGCGGTGC 840
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Sbjct 841 CATTGGCCCAAGGCTCTTCCCCACGGCTGCAAGCTGGGGGTGCAAGCTGGTGTCTACACAGG 900
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Query 1028 CCACCTCTCCAGTCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCTCTCCAGCTGC 1087
Sbjct 961 CCACCTCTCCAGTCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCTCTCCAGCTGC 1020
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Sbjct 1141 CTGCAATGGCGCTGACTTCTATGGAAACCAAGATCAGGCCCAAGATGTTCTGTGCTGGCTA 1200
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Sbjct 1261 CAGCATCTCTCGGACGCCAGCTTGGCGGCTGTGTGCGATTGTGTGATTGGGGCACTGGCTG 1320
Query 1388 TGCCCTGGCCCAAGAGCCAGGGCTCTACACCAAAGTCAGTGACTTCCGGGAGTGAGATCTCT 1447
Sbjct 1321 TGCCCTGGCCCAAGAGCCAGGGCTCTACACCAAAGTCAGTGACTTCCGGGAGTGAGATCTCT 1380
Query 1448 CCAAGCCATAAAGACTCACTCCGAGGCCAGCGGATGTTGACCCAGCTCTGA 1499
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>gb|DQ895314.2|  Synthetic construct Homo sapiens clone IMAGE:100009774; FLH183201.01L; RZPD0839H04139D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein  
Length=1294

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
(Over 10 PubMed links)

Score = 2309 bits (1250), Expect = 0.0  
Identities = 1252/1253 (99%), Gaps = 0/1253 (0%)  
Strand=Plus/Plus

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Query 245 CATGGCGCAGAAAGGAGGGTGGCCGAGCTGTGCCATGCTGCTCCAGAACCCAGATGGCAGC 304
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Sbjct 82 TCTCACTGCGGGGACCCCTGTACTTCTGACAGCCATCGGGGCGGCATCTCCGGGCCATGTT 141
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Sbjct 322 CCACTCCGAGCTGGACGTGCGAAGCGGCGGCAATGGACGTTGGGCTCTCTCTGTGTT 361
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Sbjct 382 GGACGAGGGGAGGCTGCCCCCAACCCAGAGGCTGCTGGAGGTCACTCTCGTGTGTGATGT 441
Query 665 CCCCAGAGGCCGTTTCTTGGCGGCCATCTGCCAAGACTGTGGCCGAGGAGCTGCCCGT 724
Sbjct 442 CCCCAGAGGCCGTTTCTTGGCGGCCATCTGCCAAGACTGTGGCCGAGGAGCTGCCCGT 501
Query 725 GGACCGCATCTGGGAGGCCCGGAGCACCAAGCTTGGGCGGTGGCGGTGGCAAGTCAAGCT 784
Sbjct 502 GGACCGCATCTGGGAGGCCCGGAGCACCAAGCTTGGGCGGTGGCGGTGGCAAGTCAAGCT 561
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>gb|DQ892119.2| [G] Synthetic construct clone IMAGE:100004749; FLH183205.0LX; RZPD0839H04140D  
hepsin (transmembrane protease, serine 1) (HPN)  
gene, encodes complete protein  
Length=1294

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
(Over 10 PubMed links)

Score = 2309 bits (1250), Expect = 0.0  
Identities = 1252/1253 (99%), Gaps = 0/1253 (0%)  
Strand=Plus/Plus

```

Query 245 CATGGCGCAAGAGGAGGGTGGCCGAGCTGTGCCATGCTGCTCCAGAACCCAGGTGGCAGC 304
Sbjct 22 CATGGCGCAAGAGGAGGGTGGCCGAGCTGTGCCATGCTGCTCCAGAACCCAGGTGGCAGC 81
Query 305 TCTCACTGGGGGACCCGTCTACTTCTGACAGCCATCGGGGCGGCATCTCGGGCCATGTT 364
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Sbjct 502 GGACCGCATCTGGAGAGCCCGGAGCACCAAGCTTGGGCGGTTGGCGGTGGCAAGATGACGCT 561
Query 785 TGTCTATGATGAGGACCACTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGGGTGCTGAC 844
Sbjct 562 TGTCTATGATGAGGACCACTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGGGTGCTGAC 621
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>gb|EU644753.1| Homo sapiens truncated hepsin serine protease mRNA, complete cds  
Length=1209

Score = 2228 bits (1206), Expect = 0.0  
Identities = 1206/1206 (100%), Gaps = 0/1206 (0%)  
Strand=Plus/Plus

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Query 306 CTCACGTGGGGAGCCCTGTACTTCTGACAGCCATCGGGGGCGCATCTTGGGCAATTGTG 365
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Sbjct 121 GCTGTTCTCCTCAGAGGTGACAGGAGCCGCTGTACCAAGTGCAGGTCAAGCTCTCGGAC 180
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Sbjct 661 GCGTGGCCCAAGGCTCTCCCCACGGTCTGCACTGGGGGTGCAAGGTGTGTCTACAC 720
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Sbjct 1201 TTCCAG 1206

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>emb|X07002.1|HSHEPSL  H.sapiens liver mRNA for serine protease hepsin  
Length=1199

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
(Over 10 PubMed links)

Score = 2215 bits (1199), Expect = 0.0  
Identities = 1199/1199 (100%), Gaps = 0/1199 (0%)  
Strand=Plus/Plus

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Sbjct 61 GTCAATCTCCGTGTGTGATTTGCCCCAGAGGCGCGTTTCTTGGCGCCATCTTCCAGAGATCTGT 120
Query 705 GCGCGCAGGAAGCTGTGCCGTGTGACCCGATCGTGGAGGCGCGGGAACACCAAGCTTGGGCGGG 764
Sbjct 121 GCGCGCAGGAAGCTGTGCCGTGTGACCCGATCGTGGAGGCGCGGGAACACCAAGCTTGGGCGGG 180
Query 765 TGGCCGTGGCAAGTCAGGCTTTCGCTATGATGGAGCACAACCTCTGTGGGGATCCCTGCTCT 824
Sbjct 181 TGGCCGTGGCAAGTCAGGCTTTCGCTATGATGGAGCACAACCTCTGTGGGGATCCCTGCTCT 240
Query 825 TCCGGGGACTGGGTGTGACACCGGCCCATCTGCTTCCCGAGAGCGGAACCGGGTCTCTGTCC 884
Sbjct 241 TCCGGGGACTGGGTGTGACACCGGCCCATCTGCTTCCCGAGAGCGGAACCGGGTCTCTGTCC 300
Query 885 CGATGGCGAGTGTGTTGGCGGTGCGCTGGCCAGGCGCTCTCCCAACGATCTGCAGCTGGGG 944
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Query 945 GTGCAGGCTGTGGTCTACCAACGGGGGCTATCTTCCCTTTCCGGGAACCCCAACAGCGAGGAG 1004
Sbjct 361 GTGCAGGCTGTGGTCTACCAACGGGGGCTATCTTCCCTTTCCGGGAACCCCAACAGCGAGGAG 420
Query 1005 AACAGCAACGATATTGCCCTGTGTCAACCTCTCCAGTCCCGTGCCTCTCAGAGATACATC 1064
Sbjct 421 AACAGCAACGATATTGTGCCCTGTGTCAACCTCTCCAGTCCCGTGCCTCTCAGAGATACATC 480
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Sbjct 481 CAGCGCTGTGTGCTTCCCAAGCTGCCCGGCCAGGCCCTGTGTGATGGCAAGATCTGTACCGTGT 540
Query 1125 ACGGGCTGGGGCAACACCGATGATCTATGGCCAAACAGGCGGGGATCTCCAGAGGCTCGA 1184
Sbjct 541 ACGGGCTGGGGCAACACCGATGATCTATGGCCAAACAGGCGGGGATCTCCAGAGGCTCGA 600
Query 1185 GTCCCCATTAATCAGCAATGATGTGTGCAATGGCGCTGACTTCTATGGAAACAGATCAAG 1244
Sbjct 601 GTCCCCATTAATCAGCAATGATGTGTGCAATGGCGCTGACTTCTATGGAAACAGATCAAG 660
Query 1245 CCCAAGATGTTCTGTGCTGGCTACCCCGAGGGGTGGCATTTGATGCCCTGCGAGGCGACAGC 1304
Sbjct 661 CCCAAGATGTTCTGTGCTGGCTACCCCGAGGGGTGGCATTTGATGCCCTGCGAGGCGACAGC 720

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Query 1305  GGTGGTCCCTTTGTGTGTGAAGACAGCATCTCTCGACCGCCACCGTTGGCGCGCTGTGTGGC 1364
Sbjct 721  GGTGGTCCCTTTGTGTGTGAAGACAGCATCTCTCGACCGCCACCGTTGGCGCGCTGTGTGGC 780

Query 1365  ATTGTGAGTTGGGGCACTGGCTGTGGCCCTGGCCCAAGAGCCAGGCGCTTACACCAAAAGTC 1424
Sbjct 781  ATTGTGAGTTGGGGCACTGGCTGTGGCCCTGGCCCAAGAGCCAGGCGCTTACACCAAAAGTC 840

Query 1425  AGTGACTTCGGGAGTGATGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGCATAG 1484
Sbjct 841  AGTGACTTCGGGAGTGATGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGCATAG 900

Query 1485  GTGACCCAGCTCTGACCGGGTGGCTTCTGGCTGGCGAGCGCTTCAGGGCCCGAGGTGATGCC 1544
Sbjct 901  GTGACCCAGCTCTGACCGGGTGGCTTCTGGCTGGCGAGCGCTTCAGGGCCCGAGGTGATGCC 960


Query 1545  GGTGGTGGGATCCAAGTGGGCGGAGGATGGGACGTTTTCCTCTTGGGCCCGGTGTCACA 1604
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Query 1605  GGTCCAAAGACACCCCTCCCTTCAGGGTCTCTCTTCCACAGTGGCGGGCCACTCAGGCC 1664
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Query 1665  CGAGACCAACCCACCTCAACCTCTCTGACCCCCCATGTAAATATTGTTCGTGTCTGGAC 1724
Sbjct 1081  CGAGACCAACCCACCTCAACCTCTCTGACCCCCCATGTAAATATTGTTCGTGTCTGGAC 1140

Query 1725  TCTGTCTAGGTGCCCTGATGATGGGATGCTCTTTAAATATAAAGATGGTTTGTGATTT 1783
Sbjct 1141  TCTGTCTAGGTGCCCTGATGATGGGATGCTCTTTAAATATAAAGATGGTTTGTGATTT 1199

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>db|AK233953.1|  Sus scrofa mRNA, clone:LVRM10127D02, expressed in liver  
Length=1785

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Score = 2069 bits (1120), Expect = 0.0
Identities = 1547/1750 (88%), gaps = 42/1750 (2%)
Strand=Plus/Plus

Query 66  CCACGCCACCGGCTCTGAGCTCC -AGGCCGCCGCTGCTGGCGGGC-CACCATGCTCTGCC 124
Sbjct 21  CCAC -CGCTGCCCTCTGCTCCCGGGGCC -TCCGCGCTGCGGGGC-CACCGTCTCTGCC 78

Query 125  CAGGCTTGGAGACTGA -CCC -GACCCCGGCA -C-TACCTCGAGGCTCCGCCGCCACCTGC 180
Sbjct 79  CAGGCTTGGAGACTGAACCCCTAAACCCGACCGTGTCTC -A -GCTTGGCCCCACCGCC 136

Query 181  TGGACCCCAAGGTCCCAACCTGGCCCAAGGAGTCAAGCAAGGAACTTAAACAAGAGGCA 240
Sbjct 137  CGAGCCCAAGGTCCCGCCCCGCCAGGAGGTCAAGCGGGAGTCAATTAATAGAGGCC 196

Query 241  GTGACATGGCGAGAGAGGAGGTGGCGGACGTGTGCCATGCTGTCTCGAAGCCACAGGTGG 300
Sbjct 197  GTGACATGGCGAGAGAGGAGGTGGCCAGCTGTGTATGTCTGTCTCCGAGCCACAGGTGG 256

Query 301  CAGCTCTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCGGCTATCTGGGCCA 360
Sbjct 257  CAGCTCTCACTGTGGGACCCCTGCTCTCTGACAGCCATCGGGGCGGCTCTTGGGCCA 316

Query 361  TTGTGGCTGTCTCTCTCAGAGGTGACCAAGAGCGCGTGTACCAAGTCAGAGTCAAGTCTG 420
Sbjct 317  TTGTGGCGTGTCTACTCAGAGGTGATCAAGAGCGCTGTATCTCAGTGTAGGTCTGGCCCG 376

Query 421  CGGACGCTCGGCTCATGTGTCTTGGACAGAGCGAAGGG -AGGTGGCGGCTGCTGTGTCTC 479
Sbjct 427  GGGATTCCTGGCTCAACGTTTGTATGAGAGCG -AGGGCACTGTGGCGCTCTGTGTCTC 435

Query 480  TCGCGCTCCAAAGCCAGGGTAGCCGAGCTCAGCTCGAGGAGATGGGCTTCTCTAGGAGCA 539
Sbjct 436  TCGCGCTCCAAAGCCAGGGTAGCCGAGCTCAGCTCGAGGAGATGGGCTTCTCTAGGAGCA 495

Query 540  CTGACCCACTCCAGGCTGGAGCTGGCAAGCGCGGCGCCATGGCAAGCTCGGAGCTCTCTC 599
Sbjct 496  CTGACCCACTCCAGGCTGGAGCTGGCAAGCGCGGCGCCATGGCAAGCTCGGAGCTCTCTC 555

Query 600  TGTGTGAGCAAGGGAGAGGCTGCCCCACACCCAGAGGCTGTCTGAGAGTCACTCTCGTGTGT 659
Sbjct 556  TGTGTGAGTGAAGGGAGAGGCTGCCCCAGCCAGGCGCGAGGCTGTCTGAGAGTCACTCTGTGTG 615

Query 660  GATTGCCCCAGAGGCGGCTTCTTGGCGGCCATC -TGCCAAAGACTGTGGCGCGAGAGCT 718
Sbjct 616  GACTGTCCCAAGGGGCCATTTCTGGCAACCA -CATGCCAAGACTGCGGCGATAGGAAGCT 674

Query 719  GCCCGTGGACCGCATCTGTGGAGAGCGCGGACACAGCTTGGGCCGGGTGGCCGTGGCAAGT 778
Sbjct 675  GCCCGTGGATCGCATTTGTGGCGGTTCAGGACACAGCTTGGGCCGGGTGGCCGTGGCAAGT 734

Query 775  CAGCCTTCTGCTATGATGAGACACACTCTGTGGGGATCCCTGCTCTCGGAGACTGGGT 838
Sbjct 735  CAGCTCTCTGCTATGAGAGACACACTCTGTGGGGATCCCTGCTCTCTGAGAGCTGGGT 794

Query 839  GCTGACACGCGCCCACTGCTTCCCCGAGCGGAGCCGGGTCTTCTCCGATGGCGAGTGT 898
Sbjct 795  GCTGACACGCGCCCACTGCTTCCCCGAGCGGAGCCGGGTCTTCTCCGATGGCGAGTGT 854



Query 899  TCCGGGTGCCGTGGCCAGCGCTCTCCCAAGGCTCTGACGCTGGGGGTGACGAGCTGTGGT 958

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Sbjct 855      |TTTTCCTGCTGTGGCCCAAGCACTCACCCCAGGCTGCAGATGGGGTTCAGAGCGGTGAT| 914
Query 959      CTACCAAGGAGGCTATCTTCCCTTTCTGGGACCCCAACAGCGAGGAGAAAGACACAGATAT| 1018
Sbjct 915      CTACCAATGGGAGCTATCTCCCTTTTCGAGGCCCAACAGTGAAGAGAGACAGCAATGATAT| 974
Query 1019     TGCCTCTGGTCCACCTCTCCAG-TCCCTCTGCCCCCTCAGAAATACATCCAGCCTGTGTGCC| 1077
Sbjct 975      CCGCCTGTGTCCACCTCTCCAGTCCC-TGGTCTCTCAGAAATACATCCAGCCTGTGTGCC| 1033
Query 1078     TCCAGCTGCGCGCCAGGCCCCCTGGTGGATGGCAAGATCTGTACCGTGAAGCGGTGGGCA| 1137
Sbjct 1034     TCCCGGCTGCGCGCCAGGCCCCCTGGTGGACGGCAAGATCTGCAAGGTGAAGCGGTGGGCA| 1093
Query 1138     ACAACGAGTACTATGCGCCACAGGCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCA| 1197
Sbjct 1094     ACAACGAGTACTACGCGCCACAGGCTGGGGTGTCTCCAGGAGGCGCGAGTCCCCATAATCA| 1153
Query 1198     GCAGATGATGTCTGCAATGGCGCTGACTTCTATGGAAACAGGATCAAGCCCAAGATGTCT| 1257
Sbjct 1154     GCAGTGAATGTCTGCAATGGCCCCGACTTCTACGGAAACAGGATCAAGCCCAAGATGTCT| 1213
Query 1258     GTGCTGGCTACCCCAAGGGGTGGCATTTGATGCGCTGCCAGGGGCAAGAGGGTGTTCCTTTG| 1317
Sbjct 1214     GTGCGCGCTACCCCTGAGGGGTGGCATTTGCGCTGCCAGGGGTGACAGTGTGTGCCCCCTTG| 1273
Query 1317     TGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTTGTGATTTGGG| 1377
Sbjct 1274     TGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTTGTGATTTGGG| 1333
Query 1378     GCACTGGCTGTGCCCCCTGGCCCAAGGCGGCTCTACACCAAGTCTAGTGACTTCCGGG| 1437
Sbjct 1334     GCAACGGCTGTGCCCCCTGGCCCAAGGCGGCTCTACACCAAGTCTAGTGACTTCCGGG| 1393
Query 1438     AGTGGATCTTCCAGGCCATAAAGACTCTACTCCGAAGCCAGCGGATGGTGAACCCAGCTCT| 1497
Sbjct 1394     AGTGGATCTTCCAGGCCATAAAGACTCTACTCCGAAGCCAGCGGATGGTGAACCCAGCTCT| 1453
Query 1498     GACCGGTGGCTCTT-C-GCTGCGCA-GCCTCAGGGCCCCAGGTGATCCCGGTGG-TG-| 1551
Sbjct 1454     GACCTGCGGCTTCTGTCTGCTGCGCTGCGCTCCAGGGCCCAAGCTGATCCAGTGGCTTC| 1513
Query 1552     -G-----GATC-----CAAGCTGGGCC-GAGGATGGGACGTTTCTCTCTTGGGCCCC| 1596
Sbjct 1514     AGCCCCCTCATGATGGGGTTCAACCTGGGGCGCT-GGATAGAACATTTTCTCTCTTGGGCCCC| 1572
Query 1597     GTGTCCACAGGTCCAAAGGACACCTCCCTCAGGGTCTCTCTTCCACAGTGGCGGGCCCA| 1656
Sbjct 1573     AGCCCAACAGGTCCAAAGGATACCTCCCTCCAGGTCTCTCTTCCACAGTGGCGGGCCCA| 1632
Query 1657     CTCAGCCCCGAG-ACCAACCAA-CTTCAACCTCTGACCCCAATGTAATATTTGTCTGCG| 1714
Sbjct 1633     CTCAGCCCCG-GCATCAACCCAGGCTCAACCTCTGACCCCAATGTAATATTTGTCTGCG| 1691
Query 1715     TGTCTGGGA-CTCCGCTCTAGTGGCCCCGTGATGGGATGCTCTTTTAAATATAAAGAT| 1773
Sbjct 1692     CATCTGGGGGCCCCATCTAG-TGCCCCGTGATGACAGATGCTCTTTTAAATATAAAGAT| 1750
Query 1774     GGTTTTGAATT 1783
Sbjct 1751     GGTTTTGAATT 1760

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>ref|NM\_001080241.2|  Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA  
gb|BC140636.1|  Bos taurus hepsin (transmembrane protease, serine 1), mRNA (cDNA  
clone MGC:148484 IMAGE:8196479), complete cds  
length=1919

GENE ID: 508148 HPN | hepsin (transmembrane protease, serine 1) [Bos taurus]  
(10 or fewer PubMed links)

Score = 1973 bits (1068), Expect = 0.0  
Identities = 1552/1777 (87%), Gaps = 67/1777 (3%)  
Strand=Plus/Plus

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Query 49      GCGTGGCCTAGCGAGGCCCAAGC-CA-CGCG--C-TCTGCTCCAGGCC-GCCCGCTGCT| 102
Sbjct 2       GCGAGGCTAGAGAGGCCCTCTGCGCTGCGCTGCTCTGCTCCGCTC-AGCCGCTGCGCT| 60
Query 103     GCGGGGCGCAACGATCTTCTGCGCAGGCTGGAGATGACCCGAC-CCCGGCACTA-C-CT| 159
Sbjct 61      GCGGGGCGCAACGATCTTCTGCGCAGGCTGGAGATGACCCGAC-CAACATCTCT| 119
Query 160     CGAGGCTCCGCCCCCACTGCTGGAACCCAGGGTCCCAACCTTGGCCGAGAGGTACGCCA| 219
Sbjct 120     C-AG-CTCCGCCCCCACTGCTGGAACCCAGGGTCCCAACCTTGGCCGAGAGGTACGCCG| 177
Query 228     GGGAAATCATTAACAGAGCGCTGATCTGGCGCAGAGGAGGGTGGCGGATCTGTGCCAT| 279
Sbjct 170     GGGAAATCATTAACAGAGCGCTGATCTGGCGGAGAGGAGGGTGGCGGATCTGTGCCAT| 237
Query 280     GCTGCTCCAGACCCAGGTGGCAGCTCTTCACTGCGGGGACCCGTGCTACTCTTGAACGCCA| 339
Sbjct 238     GCTGCTCCAGACCCAGGTGGCGGCTCTTCACTGTGGGAGCCGTGCTCTCTTGAACAGCA| 297
Query 340     TCGGGGCGGCATCTCGGGCCATTGTGGTGTGTTCTCTCTCAGAGGTGACCAAGAGCCGCTGT| 399

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Sbjct 298 TCGGGGCGCGCTCTCGGCCATGTGACTGTCTCACTCAGGAGTGATCAGGAGCCACTGT 357
Query 400 ACCCAAGTGCAGGTCAAGCTCTCGGACGTCGCGCTCATGCTCTTTGACAAAGCGGAGGG- 458
Sbjct 358 ATCCAGTGCAGGTCAAGCTCTCGGCCGAGATGCTCGGCTCAAGCTGTTCGACCAAGACAGA-GAGC 416
Query 459 AGCTGGCGGGCTGCTGTGCTCTCTCGCTCCAAAGCCAGGGTAGCGGACTCAGCTCGGAG 518
Sbjct 417 ACCTGGCGGCTGCTGTGCTCTCTCGCTCCAAAGCCAGGGTAGCGGACTCAGCTCGGAG 476
Query 519 GAGATGGGCTTCTCTCAGGCGCTGGA-ACCCTACCGAGCTGGAAGCTGGAAGCGCGGGCGC 577
Sbjct 477 GAGATGGGCTTCTCTCAGGCGCTTGGACTT-CTCGGAGCTGGAAGCTGGAAGCGCGGGCGC 535
Query 578 CAATGGCAAGCTCGGGCTTCTCTGTGTGGAAGAGGGGAGGCTGCCCAACACCGAGAGCT 637
Sbjct 536 CAATGGCAAGCTCGGGCTTCTCTGTGTGGAAGAGGGGAGGCTGCCCAAGCTGCCAGAGTT 595
Query 638 GCTGGAAGGTCACTCTCGGTGTGATGTGCCCAAGAGCGTTTCTTTGGCGCACTTGCCA 697
Sbjct 596 GCTCGAAGTCTCTCTCGGTGTGGAAGTGTGCCAAGAGCGTTTCTTTGGCTACCAAGTGTCCA 655
Query 698 AGACTGTGGCGCAAGAAAGCTGCCCGTGGATGCGATTTGTGGGCGCCAGACCAAGAGCT 757
Sbjct 658 AGACTGTGGCGCAAGAAAGCTGCCCGTGGATGCGATTTGTGGGCGCCAGACCAAGAGCT 715
Query 758 GGGCGGCTGGCGCTGGCAAGTCAAGCTTGTGTATGATGGAAGCACTCTCTGTGGGGGATC 817
Sbjct 716 GGGCAAGTGGCGCTGGCAAGTCAAGCTTGTGTATGATGGAAGCACTCTCTGTGGGGGATC 775
Query 817 CCTGCTCTCCGGGGA-CTGGGTGTGACAGCGCGCCCACTGCTTCCGGAGCGGAAACCGGTT 877
Sbjct 878 GTGCTCTCAAGGA-CTGGGTGTGACAGCGCGCCCACTGCTTCCGGAGCGGAAACCGGTT 835
Query 878 CTGTGCCGAAGCGAGTGTGTTGTCGGTGGCGCTGGCCCAAGCTCTTCCCAAGGTC-TGC 936
Sbjct 836 CCTATCAAGTGGCGAGTGTGTTGTCGGTGGCGCTGGCCCAAGCTCTTCCCAAGTGG-CTGTC 894
Query 937 AGCTGGGGGTGAGGCTGTGGTCTTCAACGAGGGGCTATCTTCTTTCGGAGACCCCAACA 996
Sbjct 895 AACTGGGGGTGAGGCTGTGCTCTTCAACGAGGGGCTATCTTCTTTCGGAGACCCCAACA 954
Query 997 GCGAGGAGAACAGCAACGATATGTCCTGGTCCACCTCTCCAGTC-CCCTGCCCTTCACA 1055
Sbjct 955 GCGAGGAGAAATAGCAATGACATGCGCTGGTCCACCTCTCCG-CACTGCCCTTCACA 1013
Query 1056 GAATACATCCAGCCTGTGTGCTCCAGCTGCCGCGCAAGCGCTGGTGGATGGCAAGATC 1115
Sbjct 1014 GAATACATCCAGCCGTTGTGTCTCCGCGTCCGCGGCAAGCGCTGGTGGATGGCAAGATC 1073
Query 1116 TGTACCGTGAAGGGCTGGGGCAACAGCACTACTATGGCCAACAGCGCGGGGTCTCCAG 1175
Sbjct 1074 TGGCGGTGATCTGGCTGGGGCAACAGCGCACTACTATGGCCAACAGCGCTGGGGTGTCCAG 1133
Query 1176 GAGGCTCGAGTCCCCATAACAGCAATGATGTGTGCAATGGCGCTGACTTCTATGGAAAC 1235
Sbjct 1134 GAGGCTCGAGTCCCCATAACAGCAATGATGTGTGCAATGGCGCTGACTTCTATGGAAAC 1193
Query 1236 CAGATCAAGCCCAAGATGTTCTGTGTGGCTACCCCGAGGGTGGCATGATGCTGCCAG 1295
Sbjct 1194 CAGATCAAGCCCAAGATGTTCTGTGTGGCTACCCCTGAGGGTGGCATGATGCTGCCAG 1253
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Sbjct 1254 GCGCAAGCGGTGGTCCCTTTGTGTGAGGAGAGCATCTCTCGAAGCGCAAGTTGGCGG 1313
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Sbjct 1314 CTGTGTGGCATTTGTGAGCTGGGAGCAAGCGCTGTGCCCTGGGCCAGAGCGAGGCTCTAC 1373
Query 1416 ACCAAAGTCAGTGACTTCCGGAGTGGATCTTCAGGGCCATAAAGACTCACTCGAAGGC 1475
Sbjct 1374 ACCAAAGTCAGTGACTTCCGGAGTGGATCTTCAGGGCCATAAAGACTCACTCGAAGGC 1433
Query 1476 AGCGGCAAGTGTGACCCAGCTCTGACGCGTGGCTCTCTC---GCTGCGCA-GCCTCAGAGGC 1531
Sbjct 1434 AGCGGCAAGTGTGACCCAGCTTTGACCTGTGGCTCTCTCTGCTGTGACGCTCCAGGGC 1493
Query 1532 CCGAGGTGATC-----CC---G-----GTGGTGGGATCCAGCTGGGCGGAG-ATG 1574
Sbjct 1494 CCGAGGTGATCTAAGGGGCCCCAGCCCCAGCTGATGGGGTCAAGCTGGGCGC-AGGAGTCC 1552
Query 1575 GGAAGTTTTTCTCTTGGGCGCGGTCCAGAGTCCAGAGGACACCT-CCCTCAGAGGTCC 1633
Sbjct 1553 GGAAGTTTTTCTCTTGGGCGCGGTCCAGAGTCCAGAGGACACCT-CCCTCAGAGGTCC 1612
Query 1634 TCTCTTCCACAGTGGCGGCGCCACTAGCGCCGAGCAACCCAACTCACTCCCTGAGC 1693
Sbjct 1613 TC-C-----ACGTGGCGGCGCCACTAGCGCCGAGGACCC-----TC-C-TGC-----CC 1657
Query 1694 CCCATGTAAATATTGTTCTGCTGTCTGGGA-CTCCTG-----TCTAGTGGCCCTGATG 1746
Sbjct 1658 CCCATGTAAATATTGTTCTGCTGTCTGGAATCCCGCCCGCCCACTCTG-TGCTCCGAAG 1716
Query 1747 ATGGAGTGTCTTTTAAATAAATAGATGGTTTGTGATT 1783
Sbjct 1717 ACAGGATGTCTTTTAAATAAATAGATGGTTTGTGATT 1753

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>gb|BT029913.1|  Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA, complete cds  
Length=1704

GENE ID: 508148 HPN | hepsin (transmembrane protease, serine 1) [Bos taurus]  
(10 or fewer PubMed links)

Score = 1956 bits (1059), Expect = 0.0  
Identities = 1514/1727 (87%), Gaps = 58/1727 (3%)  
Strand=Plus/Plus

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Query 91      CCGCCCGCTGCTGCAGGGGCCACCATGCTCTGCCACGGCTGGAGACTGACCC-GACCCC 149
Sbjct 2      CCGCCTGCTGCTGCAGGGGCCACCATGCTCTGCCACGGCTGGAGACTGACCTAAACCC 61
Query 150     GGCACCTA-C-CTCGAGGCTCCGCCCCCACCCTGCTGGACCCAGGGTCCACCCCTGGCCCA 207
Sbjct 62      -GCACCATCTCTC-A-GCTCCGCCCCCACCCTGCTGGAGCCAGGGTCCCGCCCGGCCCC 118
Query 208     GGAGGTGAGCCAGGGAACTATTAAACAGAGGGCAGTGACATGGCGCAGAGAGAGGGTGGCC 267
Sbjct 119     GGAGGTGAGCCAGGGAACTATTAACTAGAGGCTGTGACATGGCGCAGAGAGAGGGTGGCC 178
Query 268     GGACTGTGACCATGCTGCTCCAGACCCCAAGGTGGCAGCTCTCACTGCGGGAGCCCTGCTAC 327
Sbjct 179     GGACTGTGACCTGCTGCTCCGAGCCCAAGGTGGCAGCTCTCACTGTGGGAGCCCTGCTAC 238
Query 328     TTCTGACAGGCATCGGGGCGGATCTCGGGCCATTGTGGCTGTTCTCTCAAGAGTGACC 387
Sbjct 239     TCTTGAACAGGCATCGGGGCGAGCTCTCGGGCCATTGTGACTGTTCTCACTCAAGAGTGACC 298
Query 388     AGGAGCCCTGTATCCCACTGAGTCAAGTCAAGCTCTGCGGACGCTCGGCTCATGAGCTTTGACA 399
Sbjct 299     AAGAGCCCACTGTATCCCACTGAGTCAAGTCAAGCTCGGCGGAGTGTCTCGGCTCAAGTGTGACC 358
Query 448     AAGACGGAAGGG-ACTGGCGGCTGTCTGTGCTCTCTCGCGCTCCAAACGCAAGGTAGCGGGA 506
Sbjct 359     AACAAGA-GGGACGTGGCGCTGTCTTGTGCTCTCTCGCGCTCCAAATGCAAGGTGGCGGG 417
Query 507     CTCAGCTGCGAGGAGATGGGCTTCTCTCAGGGCCTG-ACCCACTCCAGCTGGAAGCTGCG 565
Sbjct 418     CTCAGCTGCGAGGAGATGGGCTTCTCTCAGGGCGTTGGACTT-CTCGAGCTGGAAGCTGCG 476
Query 566     AACGGCGGGCGCCATGAGCACTGCGGCTTCTTCTGTGTGGAAGAGGGAGGCTGCCCA 625
Sbjct 477     GACGGCAGGCGCCATGAGCACTGCGGCTTCTTCTGTGTGGAAGAGGGAGGCTGCCCA 536
Query 626     CACCCAGAGGCTGCTGGAGGTCACTTCGCTGTGTGATGTGCCCGAGAGCCGTCTTCTAGG 685
Sbjct 537     TGCCCCGAGGTTGCTGAGAGTCTCTTCCGTGTGCGACTGTCCAGAGAGCCGTCTTCTAGG 596
Query 686     CGCCATCTGCGCAGACTGTGGCGCGAGGAAGCTGCCCGTGGACCGCATCTGTGGAGGGCG 745
Sbjct 596     TACCACTTCCAGAGCTGTGGCCAGGAAACTGCCCGTGTGCTCATCTGTGGCGGGA 656
Query 746     GGAACACAGCTTGGGCGGGTGGCCGTGGCAAGCTCAGCCTTTCGCTATGATGAGAGCAACCT 805
Sbjct 657     GGAACACAGCTTGGGCGGGTGGCCGTGGCAAGTCAAGTCTTCTCCATGATGAGAGCAACTCT 716
Query 806     CTGTGGGGGATCCCTGCTCTTCGCGGAGCTGGGGTGTGAGCAAGCGCCCACTGCTTCCCGGA 865
Sbjct 717     CTGTGGGGGGTCCGTGCTCTCTCAGGAGCTGGGGTGTGAGCAAGCGCCCACTGCTTCCCTGA 776
Query 866     GCGGAAACCGGGTCTGTGTCGCAAGTGGCGAGTGTGTTGCGGCTGCGGTGGCGCAGAGCTCTCC 925
Sbjct 777     GCGGAAACCGGGTCTCTATCAGAGTGGCGAGTGTGTTGCGGTGCTGTGGCGCAGACTCTCAC 836
Query 926     CCAAGGCT-TGCAAGCTGGGGGTGAGGCTGTGGTCTACCAAGGGGGCTATCTTCCCTTTC 984
Sbjct 837     CCATGG-CGTGCAACTGGGGGTGAGGCTGTGATCTACCAAGGGGGCTATCTTCCCTTTC 895
Query 985     GGGACCCCAACAGCGAGGAGGAGACAGCAACGATATTGCCCTGGTCCACCTCTCAAGTC-CC 1043
Sbjct 896     GAGACCCCAACAGCGAGGAGGAGATAGCAATGACATGCGCCCTGGTCCACCTCTCCGG-CACC 954
Query 1044    CTGCCCCCTCAAGATATACATCCAGCCTGTGTGCTCCAGCTCGCGCGAGGCGCTTGAGT 1103
Sbjct 955     CTGCCCCCTCAAGATATACATCCAGCCTGTGTGCTCCCGGCTGCGCGAGGCGCTTGAGT 1014
Query 1104    GATGGCAAGACTCTGTACCGTGAAGGGCTGGGGGCAACGCAATGATATGCGCAAGAGGCC 1163
Sbjct 1015    GATGGCAAGACTCTGACCGTGAATGCGCTGGGGGCAACGCAATGATATGCGCAAGAGGCT 1074
Query 1164    GGGGTATCTCCAGAGAGGCTCCAGTCCCAATATCAGCAATGATGTCTGCAATGGCGCTTGAC 1223
Sbjct 1075    GGGGTATCTCCAGAGAGGCTCCAGTCCCAATATCAGCAATGATGTCTGCAATGGCGCTTGAC 1134
Query 1224    TTCTATTGGAACCAAGATCAAGCCCAAGATGTTCTGTGCTGGCTATCCCCGAGGGTGGCAATT 1283
Sbjct 1135    TTCTACGGGAACCAAGATCAAGCCCAAGATGTTCTGTGCTGGCTATCCCCGAGGGTGGCAATT 1194
Query 1284    GATGCTTCCAGGGCGACAGCGGTGTGCTCTTTGTGTGAGGAGACAGCATCTCTCGGACG 1343
Sbjct 1195    GATGCTTCCAGGGCGACAGTGTGTGCCCCCTTGTGTGTGAGGAGTAGCATCTCTCGGACG 1254

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Query 1344  CCAAGTTGGCGGCTGTGTGGCAATTGTGAGTTGGGGCACTGGCTGTGGCCGTGGCCAGAA 1403
Sbjct 1255  CCAAGTTGGCGGCTGTGTGGCAATTGTGAGTTGGGGCACTGGCTGTGGCCGTGGCCAGAA 1314

Query 1404  CCAGGCGTCTACACCAAAGTCACTGATCTCCGGGAGTGGATCTTCCAGGCCATAAAGACT 1463
Sbjct 1315  CCAGGCGTCTACACCAAAGTCACTGATCTCCGGGAGTGGATCTTCCAGGCCATAAAGACT 1374

Query 1464  CACTCCGAAGCCAGGCGGCACTGGTGAACCAAGCTCTGACCGGTGGCTTCTC---GCTGGCA 1520
Sbjct 1375  CACTCCGAAGCCAGGCGGCACTGGTGAACCAAGCTCTGACCGGTGGCTTCTC---GCTGGCA 1434

Query 1521  -GCCTCCAGGGCCCGAGGTGATC-----CC---G-----GTGGTGGAGTCCACGCTG 1563
Sbjct 1435  GCCTCCAGGGCCCGAGGTGATCTAAAGGGGCCCAAGCCCACTGGTGGAGTTCACCTGT 1494

Query 1564  GGCGAGG-ATGGGACGTTTCTTCTTGGGCGCGTCCACAGGTCCAGAGGACACCTT-C 1621
Sbjct 1495  GGCC-AGGGATGGAACTATTTTCTTCTTGGGCGCGGCCCCAGGTCCAGAGGATCTCTTC 1553

Query 1622  CCTCCAGGTTCTCTTCTTCCACAGTGGGGGGCCCACTCAGCCCCGAGACCAACCAACCTC 1681
Sbjct 1554  CCTCCAGGTTCTCTC---ACGTTGGGCGCGCCACTCAGCCCTGGGACCAACC---TC 1604

Query 1682  ACCCTCTGACCCCACTGTAAATATTGTCTGTCTGTCTGGACCTCTG-----TCTAGGT 1736
Sbjct 1605  -C-TGC---CCCCATGTAAATATTGTCTGTCTGTCTGGACCTCTG-----TCTAGGT 1657

Query 1737  GCGCCTGATGATGGAGTGCCTCTTTAAATAATAAAGATGGTTTGTGATT 1783
Sbjct 1658  GCTCTGAGAGACAGGATGCCTCTTTAAATAATAAAGATGGTTTGTGATT 1704

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>ref|XM\_541697.2| **U1G** PREDICTED: Canis familiaris similar to Serine protease hepsin (Transmembrane protease, serine 1) (LOC484583), mRNA  
Length=1460

GENE ID: 484583 KPN | hepsin (transmembrane protease, serine 1)  
(Canis lupus familiaris)

Score = 1873 bits (1014), Expect = 0.0  
Identities = 1322/1470 (89%), Gaps = 24/1470 (1%)  
Strand=Plus/Plus

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Query 75  CACCTCTGCTCCAGGCGCCCGCTGCTGGCGGGCCACATGCTCCTGGCCAGGCTGGA 134
Sbjct 1  CACCTCTGCTCCAGGCGCC-ACCGC--C-GCGGGGCCACCATGCTCCGCGCCAGGCTGGA 56

Query 135  GACTGACCC-GACCCCGGCACTAAGTGGGCTCCGCCCCACCTGTGGAACCCAGGTT 193
Sbjct 57  GACTGACCCGGA-GAGGGCACTATCTC-A-GCTCGCCCCACCTGCGGGAACCCAGGTT 153

Query 194  CCCACCTTGGCCAGGAGGTTCAGCCAGGGAATCATTAACAAGAGGCACTGATACGCGCA 213
Sbjct 114  CCCACCCGCGCCCGGAGGTTCAGCCCGGGAACTATTAAACAAGAGGCGCTGATACGCGGA 173

Query 254  GAAAGGAGGTTGGCCGGAATGTGACATGCTGCTCCAGACCCAGGTTGGCAGCTCTCATGCG 313
Sbjct 174  GAAAGGAGGTTGCCCCGGAATGTGACATGCTGCTCCAGACCCAGGTTGGCAGCTCTCATGCG 233

Query 314  GGGGACCCCTGCTACTTCTGACAGCCATGGGGCGGCATCTTGGGCAATTGTG-GCTGTTC 372
Sbjct 234  AGGGACCCCTGCTACTTCTGACAGGATGGGGGAGGCTCTTGGGCAATTGTGAGCT-TCC 292

Query 373  TCCTCAGGAGTGACAGAGGCGCGCTGTACCAAGTGCAGGTGAGCTCTGGGAGC-GCTGGG 431
Sbjct 293  TACTCAAGATGTATCAGAGGCCCTGTATCCGGTGCAGGCTCAGGCTTCCGCAAGCC-CGG 351

Query 432  CTCATGGTCTTTGACAGAGCGAAGGG-ACGTGGCGGCTGTGCTCTCTCGCGCTCCAA 490
Sbjct 352  CTCATGTGTGTTCAGAGCAAGCAGG-AGGGACAGTGTGGCGCTGTGTGCTCTCTCGCGCTCCAA 410

Query 491  CGCCAGGGTATGCGGACCTCAGCTGCGAGGAGTGGGCTTCTCTCAGAGGCACTGACCACTC 550
Sbjct 411  CGCCAGGGTATGCGGCGCTTCACTGCTGAGGAGATGGGCTTCTCTCAGAGGCACTGACCACTC 470

Query 551  CGAGCTGGACGTGCGAAGCGCGGGCGCCAAATGGCAAGTGGGCTTCTCTGTGTGAGAGA 610
Sbjct 471  GGAGCTGGACGTGCGAAGCGCGGGCGCCAAATGGCAAGTGGGCTTCTCTGTGTGAGAGA 530

Query 611  GGGGAGGCTGCCCCACAACCCAGAGGCTCTGAGGTCATCTCCGTGTGTGATATGGCCAG 670
Sbjct 531  GGGGAGGCTGCGGCTGGCCCGAGGCTGCTGAGGTCATCTCCGTGTGTGATATGGCCAG 590

Query 671  AGGCCGTTTCTTGGCGCGCACTGCGCAAGACTGTGGCGCGCAAGGAGCTGCCCTGGAGCCG 730
Sbjct 551  GGGCGGTTTCTTGGCTACCGTCTGCGCAAGACTGTGGCGCGCAAGGAGGAGCTGCGCTGGAGCCG 650

Query 731  CATCGTGGAGGGCCGGAACACAGCTTGGGCGCGGTGGCGGTGGCAAGTCAAGCTTCTGTA 790
Sbjct 651  CATCGTGGAGGGCCAGGACACAGGCTTGGGCGGAGTGGCCGTGGCAAGTCAAGCTTCTGTA 710

Query 791  TGATGGAGCACTACCTCTGTGG-GGATCCCTGCTCTCTCGGGGACTGGGTGCTGACAGCCG 849
Sbjct 711  CGATGGAGCACTACCTCTGTGGAGGG-TCCCTGCTGTCAGGAGCTGGGTGCTGACAGCCG 769

Query 850  CCCACTGCTTCCCGAGAGCGAAGCCGGTCTGCTGTCCGATGGCGAGTGTTCGCGGTGCGG 909

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Subjet	770	CCCCCTCTTCCCGGCGGGAACCGGCTCTCTGCTCGGGTGGCGAGTGTTCGCGCGCGCG	829
Query	910	TGGCCCAAGGCTCTTCCCAACGCTTCGACGCTGGGGGTGCGAGCTGTGGTCTACCAACGGGG	969
Subjet	830	TGGCCCAAGGCTCTTCCCAACGCTTCGACGCTGGGGGTGCGAGCACTAGTATTCACCAAGGG	889
Query	970	GCTATCTCTCTTCGGGAGCCCAACGACGACGACGACGACGACGACATATTCACCGCTGGTTC	1028
Subjet	890	GCTACTCTCCCTTTCGAGAGCCCAACGACGAGGAGGAAAAACGACATGACATGCCCCTGGTTC	949
Query	1030	ACCTCTCCAGTTCCTCCGCTCCCTCTACAGATACATCCAGCTCTGTGTGCTCCCACTGTCGG	1089
Subjet	950	ACCTCTCCAGCTCCCTCCGCTCCCTCTACAGATACATCCAGCGCTCTGTGCTCCCGCGAGCTG	1009
Query	1090	GCCAGGCTCTGTGGATGGCAAGTCTNTACCTGTGACGGCTGGGGCAACGACGCACTACT	1149
Subjet	1010	GCCAGGCTCTGTGGATGGCAAGTCTGCAAGTGTGACCGCTGGGGCAACGACGCACTACT	1069
Query	1150	ATGGCCACACAGGCTCGGGGTATCGACGAGGCTCGAGTCCCCATAATACGCAATGATG-CTC	1208
Subjet	1070	ACGCCCAACAGGCTTGGGTGTCTCCAGGAGCGCGGAGTCCCCATCATGCAACAAG-CTC	1128
Query	1209	TGCAATGGGCGTCTTCTATGT-AAAACAGATCAAGCCAGATGTTCTGTGTGGGCTA	1267
Subjet	1129	TGCAACGGCCCGACTCTTACGCGAAA-CCAAGTCAAGCCCAAGATGTCTGTGCGCGCTA	1187
Query	1268	CCCGAGGGGTGGCATTGATGCTGCGAGGGGACAGCGGTGTGCTCCCTTCTGTGTGTAGGA	1327
Subjet	1188	CCCGAGGGGCGCATCGATGCTGCGAGGGGACAGCGGTGTGCTCCCTTCTGTGTGTAGGA	1247
Query	1328	CAGCATCTCTCGAGCGCCACAGTGTGGCGCTGTGTGGCATGTGAATGTGGGCGACTGGCTG	1387
Subjet	1248	CAGCATCTCTCGAGCGCCACAGTGTGGCGCTGTGTGGCATGTGAATGTGGGCGACTGGCTG	1307
Query	1388	TGCCCTGGCCAGAGACCGACGGGTCTACACCAAGTCACTGACTCTCGGGAGTGGATCTT	1447
Subjet	1308	TGCCCTGGCCAGAGACCGACTGTCTACACCAAGTCACTGACTCTCGGGAGTGGATCTT	1367
Query	1448	CACAGCGCAAAAGTCACTTCGAGAGCGACGCGCATGATGACCAAGCATCTGACCGCTGGCC	1507
Subjet	1368	CACAGCGCAAAAGTCTACCTCGAGAGCGCGCATGATGACCAAGCATCTGACCGCTGGCC	1427
Query	1508	TTCTCT--CTCGTGGC-GCCTCGAGGCC 1533	
Subjet	1428	TGTGCTCTGATGGGCTCTCTCGAGGCC 1457	

>ref|XM\_001157575.1| G PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA  
Length=1695

GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)  
[Pan troglodytes]

Sort alignments for this subject sequence by:

E value	Score	Percent identity	Query start position	Subject start position
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Score = 1866 bits (1011), Expect = 0.0	
Identities = 1015/1017 (99%), Gaps = 0/1017 (0%)	
Strand=Plus/Plus	
Query	191 GGTCCCAACCCCTGGCCAGGAGGTTCAGCCAGGAAATCATTAACAAGAGGCAGTGAATGCG 250
Sbjct	146 GGTCCCAACCCCTGGCCAGGAGGTTCAGCCAGGAAATCATTAACAAGAGGCAGTGAATGCG 205
Query	251 GCAGAGAGGAGGTGGCCCGGATCTGTGCCATGCTGCTTCAGAGCCCAAGTGTGACGCTCTCAC 310
Sbjct	206 GCAGAGAGGAGGTGGCCCGGATCTGTGCCATGCTGCTTCAGAGCCCAAGTGTGACGCTCTCAC 265
Query	311 TGCGGGAGACCCCTCTACTCTTCAGAGCCATCGGGGCGGACATCTGGGCGCAATTGTGGCTGT 370
Sbjct	266 TGCGGGAGACCCCTCTACTCTTCAGAGCCATCGGGGCGGACATCTGGGCGCAATTGTGGCTGT 325
Query	371 TCTCCTCAGAGGTGACAGGAGGACCGCTTATACCAATGTCAGAGTCAGCTCTGCGGAGCGCTCG 385
Sbjct	326 TCTCCTCAGAGGTGACAGGAGGACCGCTTATACCAATGTCAGAGTCAGCTCTGCGGAGCGCTCG 380
Query	431 GCTCATGAGTCTTTTGAAGAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 490
Sbjct	386 GCTCATGAGTCTTTTGAAGAAG 445
Query	491 CGCAGAGGTAGCCCGGATCTAGTCTCGAGAGATAGAGGCTTCTTCAGAGGACATGACCACTC 505
Sbjct	446 CGCAGAGGTAGCCCGGATCTAGTCTCGAGAGATAGAGGCTTCTTCAGAGGACATGACCACTC 500
Query	551 CAGATCGAGCTGTGACGACGCGCGGCGCCATATGCACTGTGGGCTCTCTCTGCTGTGAGACGA 610
Sbjct	506 CAGATCGAGCTGTGACGACGCGCGGCGCCATATGCACTGTGGGCTCTCTCTGCTGTGAGACGA 565
Query	611 GGGAGAGGCTGCGCCCAACACCGAGAGCTGCTGAGAGTCACTCTCGTGTGTGATGTGCCCCAG 670
Sbjct	566 GGGAGAGGCTGCGCCCAACACCGAGAGCTGCTGAGAGTCACTCTCGTGTGTGATGTGCCCCAG 625
Query	671 AGGCCGCTTTCTTGGCCGCCCATCTGCCAGACTGTGGCCGACAGGAAGCTGACCTGGTGGACCG 730

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Sbjct 626 AGGCCGTTTCTTGCCCGCCATCTGCCAAGACTGTGCGCCGACGAGCTGCCCGTGACCG 685
Query 731 CATCGTGGAGGCGCGGACACAGCTTGGCGCGGTGGCGAGTGCAGCCTTCGCTA 790
Sbjct 686 CATCGTGGAGGCGCGGACACAGCTTGGCGCGGTGGCGAGTGCAGCCTTCGCTA 745
Query 791 TGATGGAGACACCTCTGTGGGGATCCCTGCTCTCCGGGACCTGGTGCTGACAGCGC 850
Sbjct 746 TGATGGAGACACCTCTGTGGGGATCCCTGCTCTCCGGGACCTGGTGCTGACAGCGC 805
Query 851 CCACTGCTTCCCGGAGCGAGAACGGGTCTGTCCGATGGCGAGTGTTCGCGGTGCCGT 910
Sbjct 806 CCACTGCTTCCCGGAGCGAGAACGGGTCTGTCCGATGGCGAGTGTTCGCGGTGCCGT 865
Query 911 GGCCTCAGGCTCTCCCAACGGTCTGCGAGTGGGGGTGCAAGCTGTGGTCTACACAGGGGG 970
Sbjct 866 GGCCTCAGGCTCTCCCAACGGTCTGCGAGTGGGGGTGCAAGCTGTGGTCTACACAGGGGG 925
Query 971 CTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTCGCGTGTCCA 1030
Sbjct 926 CTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTCGCGTGTCCA 985
Query 1031 CCTCTCCAGTCCCTGCCCTCAGAGATACATCCAGCCTGTGTGCTCCAGCTGCCGG 1090
Sbjct 986 CCTCTCCAGTCCCTGCCCTCAGAGATACATCCAGCCTGTGTGCTCCAGCTGCCGG 1045
Query 1091 CCAGGCGCTGGTGGATGCGAGATCTGTACCGTGAACGGGCTGGGGCAACAGCGAGTACTA 1150
Sbjct 1046 CCAGGCGCTGGTGGATGCGAGATCTGTACCGTGAACGGGCTGGGGCAACAGCGAGTACTA 1105
Query 1151 TGGCCCAACAGGCGCGGGTACTCCAGGAGGCTGAGTCCCAATACAGCAATGATGT 1207
Sbjct 1106 TGGCCCAACAGGCGCGGGTACTCCAGGAGGCTGAGTCCCAATACAGCAATGATGT 1162


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Score = 968 bits (524), Expect = 0.0  
 Identities = 528/530 (99%), Gaps = 0/530 (0%)  
 Strand=Plus/Plus

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Query 1254 TTCTGTGCTGGCTACCCCGAGGTTGGCATTGATGCTGCCAGGGCGACAGCGTGTGCC 1313
Sbjct 1164 TTCTGTGCTGGCTACCCCGAGGTTGGCATTGATGCTGCCAGGGCGACAGCGTGTGCC 1223
Query 1314 TTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTTGTGAGT 1373
Sbjct 1224 TTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTTGTGAGT 1283
Query 1374 TGGGGCACTGGCTGTGCCCTGGCCGAGAGCGAGCGCTCTACACAAAGTCATGACTTTC 1433
Sbjct 1284 TGGGGCACTGGCTGTGCCCTGGCCGAGAGCGAGCGCTCTACACAAAGTCATGACTTTC 1343
Query 1434 CGGGAGTGGATCTTCCAGGCTATAAAGACTCACTCCGAAAGCGAGCGCATGTGTGACCCAG 1493
Sbjct 1344 CGGGAGTGGATCTTCCAGGCTATAAAGACTCACTCCGAAAGCGAGCGCATGTGTGACCCAG 1403
Query 1494 CTCTGACCGGTGGCTTCTGCGCTGCGCAGCTCCAGGGCCCGAGGTGATCCCGGTGGTGGG 1553
Sbjct 1404 CTCTGACCGGTGGCTTCTGCGCTGCGCAGCTCCAGGGCCCGAGGTGATCCCGGTGGTGGG 1463
Query 1554 ATCCACGCTGGGCGGAGATGGGACGTTTTTCTTCTTGGGCGCGGCTCCAGACGTCGAAG 1613
Sbjct 1464 ATCCACGCTGGGCGGAGATGGGACGTTTTTCTTCTTGGGCGCGGCTCCAGACGTCGAAG 1523
Query 1614 ACACCTTCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTGAGCCCGAGACAC 1673
Sbjct 1524 ACACCTTCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTGAGCCCGAGACAC 1583
Query 1674 CCACACCTCACCCCTCTGACCCCATGTAATAATTTGTTCTGCTGTCTGGGACTCTGTCTA 1733
Sbjct 1584 CCACACCTCACCCCTCTGACCCCATGTAATAATTTGTTCTGCTGTCTGGGACTCTGTCTA 1643
Query 1734 GGTGCCCTTGATGATGGGATGCTCTTTAAATAATAAGATGGTTTGTGATT 1783
Sbjct 1644 GGTGCCCTTGATGATGGGATGCTCTTTAAATAATAAGATGGTTTGTGATT 1693

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>emb[CR59717.1]  full-length cDNA clone CS0DJ0031L08 of T cells (Jurkat cell line)  
 Cot 10-normalized of Homo sapiens (human)  
 Length=1828

GENE ID: 3249 HFN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
 (Over 10 PubMed links)

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 1714 bits (928), Expect = 0.0  
 Identities = 928/928 (100%), Gaps = 0/928 (0%)  
 Strand=Plus/Plus

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Query 533 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGCGG 592
Sbjct 375 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGCGG 434
Query 593 CTCTCTCTGTGTGGAACAGAGGAGGGCTGCCCAACACCAAGAGGCTGCTGAGAGTCACTCT 652

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Sbjct 435 CTTCTTCGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGCTGTGGAGGTCATCTC 494  
 Query 653 CGTGTGTGATTGCCCCAGAGGCGTTTCTTGGCCGCATCTGCCAAGACTGTGGCCGCGAG 712  
 Sbjct 495 CTPGTGTGATTGCCCCAGAGGCGTTTCTTGGCCGCATCTGCCAAGACTGTGGCCGCGAG 554  
 Query 713 GAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAAGCTTGGGCGCGTGGCCGTG 772  
 Sbjct 555 GAAGCTGCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAAGCTTGGGCGCGTGGCCGTG 614  
 Query 773 GCAGGTGAGCCTTCTGCTATGATGAGACACACTCTGTGGGGGATCCTGCTCTCCGCGGA 832  
 Sbjct 615 GCAGGTGAGCCTTCTGCTATGATGAGACACACTCTGTGGGGGATCCTGCTCTCCGCGGA 674  
 Query 833 CTGGGTGCTGACAGCGCGCCCACTGCTCTCCGAGAGCGGAAACCGGCTCTGTCCTGATGGCG 892  
 Sbjct 675 CTGGGTGCTGACAGCGCGCCCACTGCTCTCCGAGAGCGGAAACCGGCTCTGTCCTGATGGCG 734  
 Query 893 AGTGTATTGCCGAGTGCCTGGCCAGGCTCTCCCCACGGTCTGCAAGCTGGGGGTGACAGGC 952  
 Sbjct 735 AGTGTATTGCCGAGTGCCTGGCCAGGCTCTCCCCACGGTCTGCAAGCTGGGGGTGACAGGC 794  
 Query 953 TGTGGTCTACACAGGGGGCTATCTTCCCTTTTGGGAGCCCAACAGCGAGGAGAACAGCAA 1012  
 Sbjct 795 TGTGGTCTACACAGGGGGCTATCTTCCCTTTTGGGAGCCCAACAGCGAGGAGAACAGCAA 854  
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 Query 1073 GTGGCTCCAGGCTGCCGCGCAGGGCCCTGGTGGATGGCAAGATCTGTACCGTGAAGGGCTG 1132  
 Sbjct 915 GTGGCTCCAGGCTGCCGCGCAGGGCCCTGGTGGATGGCAAGATCTGTACCGTGAAGGGCTG 974  
 Query 1133 GGGCAACACGACGATCTATGCGCAAGCGCGGGGTACTCCAGGAGGCTCGAGTCCCAT 1192  
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 Query 1193 AATCAGCAATGATGTCTGCAATGGCCGTGACTTCTATGAGAAACAGGATCAAGCCCAAGAT 1252  
 Sbjct 1035 AATCAGCAATGATGTCTGCAATGGCCGTGACTTCTATGAGAAACAGGATCAAGCCCAAGAT 1094  
 Query 1253 GTTCTGTGCTGGTCTACCCCGAGGGTGGCATTTGATGCCCTGCCAGGGCGACAGCGGTGCTC 1312  
 Sbjct 1095 GTTCTGTGCTGGTCTACCCCGAGGGTGGCATTTGATGCCCTGCCAGGGCGACAGCGGTGCTC 1154  
 Query 1313 CTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCAATTGTAG 1372  
 Sbjct 1155 CTTTGTGTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCAATTGTAG 1214  
 Query 1373 TTGGGGCACTGGCTGTGCCCTGGCCGAGGAGCCAGGCGTCTACACAAAGTCACTGATCTT 1432  
 Sbjct 1215 TTGGGGCACTGGCTGTGCCCTGGCCGAGGAGCCAGGCGTCTACACAAAGTCACTGATCTT 1274  
 Query 1433 CCGGAGATGGATCTTCCAGGCCATAAAG 1460  
 Sbjct 1275 CCGGAGATGGATCTTCCAGGCCATAAAG 1302

Score = 566 bits (306), Expect = 1e-157  
 Identities = 210/312 (95%), Gaps = 0/312 (0%)  
 Strand=Plus/Plus

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 Sbjct 1517 AGACTCACTCCGAAGCCAGCGGATGGTGAACCCAGCTCTGACCGGTGGCTTCTGCTGG 1576  
 Query 1519 CAGGCTCCAGGGCCGAGGTGATCCCGGTGGTGGATCCACGCTGGGCGAGATGGGAC 1578  
 Sbjct 1577 CAGGCTCCAGGGCCGAGGTGATCCCGGTGGTGGATCCACGCTGGGCGAGATGGGAC 1636  
 Query 1579 GTTTTTCTCTTGGGCGCGGTCCACAGGTCCAAAGGACACCCCTCCCTCCAGGGTCTCTCT 1638  
 Sbjct 1637 GTTTTTCTCTTGGGCGCGGTCCACAGGTCCAAAGGACACCCCTCCCTCCAGGGTCTCTCT 1696  
 Query 1639 TCCACAGTGGCGGGCCCACTCAGCCCGAGGACACCCAACTCAACCTCTGAGACCCCAT 1698  
 Sbjct 1697 TCCACAGTGGCGGGCCCACTCAGCCCGAGGACACCCAACTCAACCTCTGAGACCCCAT 1756  
 Query 1699 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758  
 Sbjct 1757 GTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1816  
 Query 1759 TTAATAATAA 1770  
 Sbjct 1817 TTAATAATAA 1828

Score = 326 bits (176), Expect = 3e-85  
 Identities = 176/176 (100%), Gaps = 0/176 (0%)  
 Strand=Plus/Plus


Query 86 CCAGGCCGCGCCGCTGCTGCGGGGCCACCATGCTCTCTGCCAGGCTGGAGACTGACCGA 145  
 Sbjct 1 CCAGGCCGCGCCGCTGCTGCGGGGCCACCATGCTCTCTGCCAGGCTGGAGACTGACCGA 60  
 Query 146 CCCCGGCACTACCTCGAGGCTCCGCCCCCACTGCTGGACCCAGGGTCCCACTCTGGCC 205



Sbjct 61 CCCCGGCACTACCTCGAGGCTCCGCCCCCACTGTGAGCCCAAGGTCACCCCTGGCC 120  
 Query 206 CAGGAGGTGAGCCAGGGAATCATTAACAAGAGGCACTGACATGGCCAGAGGAGG 261  
 Sbjct 121 CAGGAGGTGAGCCAGGGAATCATTAACAAGAGGCACTGACATGGCCAGAGGAGG 176

Score = 244 bits (132), Expect = 8e-61  
 Identities = 132/132 (100%), Gaps = 0/132 (0%)  
 Strand=Plus/Plus

Query 405 GTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGACGTGG 464  
 Sbjct 176 GTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGACGTGG 235  
 Query 465 CGGCTGCTGTGCTCTCGCGCTCCAAAGCCAGGGTAGCCGGACTCAGCTCGAGGAGGATG 524  
 Sbjct 236 CGGCTGCTGTGCTCTCGCGCTCCAAAGCCAGGGTAGCCGGACTCAGCTCGAGGAGGATG 295  
 Query 525 GGCTTCCTCAGG 536  
 Sbjct 296 GGCTTCCTCAGG 307

>emb|CR592189.1|  full-length cDNA clone CS0DM012Y015 of Fetal liver of Homo sapiens (human)  
 Length=1212

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
 (Over 10 PubMed links)

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 1663 bits (900), Expect = 0.0  
 Identities = 911/916 (99%), Gaps = 2/916 (0%)  
 Strand=Plus/Plus

Query 856 GCTTCC-CGGAGCGGAACCGGCTCTGTCCCGATGGCGAGTGTTGGCCGGTGCGTGCC 914  
 Sbjct 298 GCTTCTCAG-CCGGAACCGGCTCTGTCCCGATGGCGAGTGTTGGCCGGTGCGTGCC 356  
 Query 915 CAGAGCTCTCCCAAGGTCGAGCTGGGGGTGAGGCTGGGTCTACCAAGCGGGCTAT 974  
 Sbjct 357 CAGAGCTCTCCCAAGGTCGAGCTGGGGGTGAGGCTGGGTCTACCAAGCGGGCTAT 416  
 Query 975 CTTCGCTTTTCGGAACCCCAACAGCGAGGAGAACAGCAAGATATTGCCCTGGTCCACCTC 1034  
 Sbjct 417 CTTCGCTTTTCGGAACCCCAACAGCGAGGAGAACAGCAAGATATTGCCCTGGTCCACCTC 476  
 Query 1035 TCCAGTCCCCTGCCCCCTCAGAAATACATCCAGGCTGTGTGACCTCCAGCTGCGCGCAG 1094  
 Sbjct 477 TCCAGTCCCCTGCCCCCTCAGAAATACATCCAGGCTGTGTGACCTCCAGCTGCGCGCAG 536  
 Query 1095 GCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACAGCAGTACTATGGC 1154  
 Sbjct 537 GCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACAGCAGTACTATGGC 596  
 Query 1155 CAAACAGGCCCGGGGTATCTCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAT 1214  
 Sbjct 597 CAAACAGGCCCGGGGTATCTCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAT 656  
 Query 1215 GGCCTGACTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTGGCTCGACATC 1274  
 Sbjct 657 GGCCTGACTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTGGCTCGACATC 716  
 Query 1275 GGTGGCATTGATGCTGCGAGGGGAGCAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATC 1334  
 Sbjct 717 GGTGGCATTGATGCTGCGAGGGGAGCAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATC 776  
 Query 1335 TCTCGAGCGCCAGCTTGGCGGCTGTGTGTGAGTGTGAGTGTGGGACATCGCTGTGCCCTG 1394  
 Sbjct 777 TCTCGAGCGCCAGCTTGGCGGCTGTGTGTGAGTGTGAGTGTGGGACATCGCTGTGCCCTG 836  
 Query 1395 GCCCAGAGGCCAGGCGCTTACACCAAGTCAGTGACTTCCGGAATGGATCTTCCAGGCC 1454  
 Sbjct 837 GCCCAGAGGCCAGGCGCTTACACCAAGTCAGTGACTTCCGGAATGGATCTTCCAGGCC 896  
 Query 1455 ATAAAGACTCACTCCGAAGCCAGCGGCAATGTTGACCCAGCTCTGACCGGTGGCTTCTGCG 1514  
 Sbjct 897 ATAAAGACTCACTCCGAAGCCAGCGGCAATGTTGACCCAGCTCTGACCGGTGGCTTCTGCG 956  
 Query 1515 TGGCGAGCTCCAGGGGCCAGGTGATCCCGGTGGTGGGATCCAAGTGGGCGGAGGATG 1574  
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 Sbjct 1017 GGAAGTTTCTTCTTCTTGGGCGCCGCTCCACAGGTCCAAGGACACCCCTCCCTCAGGGTCT 1076  
 Query 1635 CTCTTCCACAGTGGCGGGGCCACTCAGCCCGGAGACACCCAACTCACCCTCTGAGACC 1694  
 Sbjct 1077 CTCTTCCACAGTGGCGGGGCCACTCAGCCCGGAGACACCCAACTCACCCTCTGAGACC 1136  
 Query 1695 CCATGTAAATATTGTTCTGCTGTCTGGGACTCCCTGTCTAGGTGCCCTGATGATGGGATG 1754

Sbjct 1137 CCATGTAAATATTGTTCTGCTGTCTG93ACTCTCTGTCTAGGTGCCCCGTAGTACGGGATG 1196  
 Query 1755 CTTCTTAAATAATAAA 1770  
 Sbjct 1197 CTTCTTAAATAATAAA 1212

Score = 327 bits (177), Expect = 8e-86  
 Identities = 177/177 (100%), Gaps = 0/177 (0%)  
 Strand=Plus/Plus

Query 85 TCCAGGCGCGCCGCTGCTGCGGGGCAACCATGCTCTGCCCAGGCGCTGGAAGCTGACCGG 144  
 Sbjct 1 TCCAGGCGCGCCGCTGCTGCGGGGCAACCATGCTCTGCCCAGGCGCTGGAAGCTGACCGG 60  
 Query 145 ACCCCGGCACTACTCGAGGCTCGCGCCCCCACTGCTGGAACCCAGGGTCCCAACCTGTGC 204  
 Sbjct 61 ACCCCGGCACTACTCGAGGCTCGCGCCCCCACTGCTGGAACCCAGGGTCCCAACCTGTGC 120  
 Query 205 CCAGGAGGTGACGCCAAGGAATCATTAACAAGAGGCACTGACATGGCGCAGAGAGAGG 261  
 Sbjct 121 CCAGGAGGTGACGCCAAGGAATCATTAACAAGAGGCACTGACATGGCGCAGAGAGAGG 177

Score = 244 bits (132), Expect = 8e-61  
 Identities = 132/132 (100%), Gaps = 0/132 (0%)  
 Strand=Plus/Plus

Query 405 GTGCAAGGTGAGCTCTGCGGACGCTCGGCTCATGCTCTTTGACAAGACGGAAGGAGCTGG 464  
 Sbjct 177 GTGCAAGGTGAGCTCTGCGGACGCTCGGCTCATGCTCTTTGACAAGACGGAAGGAGCTGG 236  
 Query 465 CGGCTGCTGTGCTCTCTCGCGCTCCAAAGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATG 524  
 Sbjct 237 CGGCTGCTGTGCTCTCTCGCGCTCCAAAGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATG 296  
 Query 525 GGCTTCTCTCAGG 536  
 Sbjct 297 GGCTTCTCTCAGG 308

>emb|CU693029.1| Synthetic construct Homo sapiens gateway clone IMAGE:100019300  
 3' read HPM mRNA  
 Length=1484

Score = 1653 bits (895), Expect = 0.0  
 Identities = 1070/1151 (92%), Gaps = 26/1151 (2%)  
 Strand=Plus/Minus

Query 355 GGGC-CATTGTGGCTGTTCTCTCAGGAGTGAC-CAGGAGCCGCTG-TACCCAGTGCAAG 411  
 Sbjct 1148 GGGCACATGTTGGGT-TTTTCTCGGAG-GGACAGGAGCC-CTGTA-CCAGGGAGG 1093  
 Query 412 TCAGCTCTCGGACG-CTC-GGCTCATGGTCTTTGACAAGACGGAAGGAGCT-GGCGGC 468  
 Sbjct 1092 TTAACITTG-GGA-GCCTCGGGTTC-AAGTTTTCACAAACGGAAGGAGC-TGGGGGT 1037  
 Query 469 TGCTGTGCTCTCTCGCGCTCCAAAGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCT 528  
 Sbjct 1039 TTTTGT-TTCTTG-GGTTCAACCCAGGGAACCCGGA-TTAGCTGCAAGGA-AT-GGCT 982  
 Query 529 TCTCTAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACCGCGGCGCCATGCGACGT 588  
 Sbjct 981 TGCTCAAGGGA-TGACCCGCTCCGAG-GGGACGTGGGACCGCGGCGCCCAATGGCAC-T 925  
 Query 589 CGGGCTTCTTCTGTGTGACGAGGGGAGGGCTGCCCCACCCAGAGGCTGTGAGAGTCA 648  
 Sbjct 984 TGGGGTTTTCTTG-GGGGACGAGGGAAGGCT-CCCCAGACCCAGAGGCGGCTGAGAGTCA 867  
 Query 649 TCTCCGTGTGTG-ATTGCCCGAGAGGCGTCTTCTTGGCGGCCATCTGCCAGACTGTGGC 707  
 Sbjct 866 TCTTCG-GGGGATATGCCCCGAGGCGGCTTGTGGCGCCCATCTGCCAGACTGTGGC 808  
 Query 708 CGCAGGAGAGCTGCCCGTGGACGCACTGTGGGAGGCGCGGACCACTGCTGGGCGGTGG 767  
 Sbjct 807 CGCAGGAGAGCTGCCCGTGGGCGCATGTGGGAGGCGCGGAGCCGACCTTGGGCGGTGG 748  
 Query 768 CCGTGGCAAGTCAAGCTTTGCGTATGATGAGACCACTCTGTGGGGATCCCTGCTCTCC 827  
 Sbjct 747 CCGTGGCAAGTCAAGCTTTGCGTATGATGAGGACCACTCTGTGGGGATCCCTGCTCTCC 688  
 Query 828 GGGAGCTGGGTGTGACAGCGCGCCACTGCTCTCCCGAGGCGGACCGGCTCTGCTCCGA 887  
 Sbjct 628 GGGAGCTGGGTGTGACAGCGCGCCACTGCTCTCCCGAGGCGGACCGGCTCTGCTCCGA 628  
 Query 888 TGGCGAGTGTGTTGCGGCTGGCGGTGGCCGAGGCTCTCCCCACGGTCTGCGAGCTGGGGTG 947  
 Sbjct 627 TGGCGAGTGTGTTGCGGCTGGCGGTGGCCGAGGCTCTCCCCACGGTCTGCGAGCTGGGGTG 568  
 Query 948 CAGGCTGTGGTCTACCAAGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAC 1007  
 Sbjct 567 CAGGCTGTGGTCTACCAAGGGGCTATCTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAC 508  
 Query 1008 AGCAACGATATTGCCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCAGAGAAATACATCCAG 1067  
 Sbjct 507 AGCAACGATATTGCCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCAGAGAAATACATCCAG 448  
 Query 1068 CCTGTGTGCTCCAGCTGCGGGCAGGCGCTGGTGGATGGCAAGATCTGTACCGGTGACG 1127

Sbjct	447	CCCTGTGTGCTCCCAAGCTGCTCCGGCCAGGGCCCTGGTGGATGGCAGAGTCTGTATCCGTGACG	388
Query	1128	GGCTGGGGCAACAGCGCTACTATGTGGCAACAGGGCCGGGTACTCTCAGAGAGGCTCGAGTCT	1187
Sbjct	387	CCCTGTGTGCTCCCAAGCTGCTCCGGCCAGGGCCCTGGTGGATGGCAGAGTCTGTATCCGTGACG	328
Query	1188	CCCATATCATCAGCAATGATGTGCTGCAATGGCGCTGACTCTATGGAAGACAGATCAAGGCC	1247
Sbjct	327	CCCATATCATCAGCAATGATGTGCTGCAATGGCGCTGACTCTATGGAAGACAGATCAAGGCC	268
Query	1248	AAGATGTTCTTGCTCTGGTCAACCCGAGGGTGGCAATTGATGCTCTGCAGGGGCGACAGCGGT	1307
Sbjct	267	AAGATGTTCTTGCTCTGGTCAACCCGAGGGTGGCAATTGATGCTCTGCAGGGGCGACAGCGGT	207
Query	1308	GTGCTCCCTTTGTGTGTGAGGACAGCATCTCTCGGAGCGCACTGTGGCGGCTGTGTGGCAATT	1367
Sbjct	207	GTGCTCCCTTTGTGTGTGAGGACAGCATCTCTCGGAGCGCACTGTGGCGGCTGTGTGGCAATT	148
Query	1368	GTGAGTTGGGGCACTGGCTGTGCCCTG3CCCAAGGACAGGCGCTATACCAAAAGTCAGT	1427
Sbjct	147	GTGAGTTGGGGCACTGGCTGTGCCCTG3CCCAAGGACAGGCGCTATACCAAAAGTCAGT	88
Query	1428	GACTCTCGGAGTGAGTCTTCGAGCGCATTAAGACTCACTCGAAGACAGCGCGGATGCTG	1487
Sbjct	87	GACTCTCGGAGTGAGTCTTCGAGCGCATTAAGACTCACTCGAAGACAGCGCGGATGCTG	28
Query	1488	ACCCAGCTCTG 1498	
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>ref|XM_001157514.1| G PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine
1), transcript variant 1 (HPN), mRNA
Length=2104
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GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)  
[Pan troglodytes]

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 1476 bits (799), Expect = 0.0  
Identities = 803/805 (99%), Gaps = 0/805 (0%)  
Strand=Plus/Plus

Query	403	CAGTGCAGTTCAGCTCTCGGACGCGCTCGGCTCATGGTCTTTGACAGACGGAAGGAGCGT	462
Sbjct	767	CAGTCGACAGCTCAGCTCTCGGACGCGCTCGGCTCATGGTCTTTGACAGACGGAAGGAGCGT	826
Query	463	GGCGCGTCTGTGTCTCTCGGCGCTCCACGCCAGGGTACCGGATCTAGTCGCGAGGAGA	522
Sbjct	827	GGCGCGTCTGTGTCTCTCGGCGCTCCACGCCAGGGTACCGGATCTAGTCGCGAGGAGA	886
Query	523	TGGGCTTCTCTCAGGCGACCTGACCCATCTCCAGCTGGAAGCTGCGAAGCGCGGCGCCCAATG	58
Sbjct	887	TGGGCTTCTCTCAGGCGACCTGACCCATCTCCAGCTGGAAGCTGCGAAGCGCGGCGCCCAATG	946
Query	583	GCAAGTCGCGGCTCTCTCTGTGTGGAAGCGGAGCGCTGCCCAACACCCAGAGGCTCTGTG	642
Sbjct	947	GCAAGTCGCGGCTCTCTCTGTGTGGAAGCGGAGCGCTGCCCAACACCCAGAGGCTCTGTG	1006
Query	643	AGGTCTATCTCCGTGTGTGATTGCCCAAGAGCGCGTTTCTGTGGCGCCCATCTGCGACAAGACT	702
Sbjct	1007	AGGTCTATCTCCGTGTGTGATTGCCCAAGAGCGCGTTTCTGTGGCGCCCATCTGCGACAAGACT	1066
Query	703	GTGGCCGCGAGGAAGCTGCCCGTGGACCGCATGTGTGGAGAGCGCGGAGACCAAGCTTGGGCC	762
Sbjct	1067	GTGGCCGCGAGGAAGCTGCCCGTGGACCGCATGTGTGGAGAGCGCGGAGACCAAGCTTGGGCC	1126
Query	763	GTGGAGCGTGGCAAGTCAAGCTTGTGATATGTGAGGACCAACTCTGTGTGGGGATGCGGC	822
Sbjct	1127	GTGGAGCGTGGCAAGTCAAGCTTGTGATATGTGAGGACCAACTCTGTGTGGGGATGCGGC	886
Query	823	TCTTCGCGGAGCTTGGGTGTGAGCAAGCGCCACTGTCTCCGCGAGCGGAAAGCGCTCTGT	882
Sbjct	1187	TCTTCGCGGAGCTTGGGTGTGAGCAAGCGCCACTGTCTCCGCGAGCGGAAAGCGCTCTGT	946
Query	883	CCCGATGGGAGATGTTGACCGTGTCCGTGACCAGGCTCTCTCCCAACGCTGTGCACTGTG	942
Sbjct	1247	CCCGATGGGAGATGTTGACCGTGTCCGTGACCAGGCTCTCTCCCAACGCTGTGCACTGTG	1006
Query	943	GGGTGACAGCTTGTGGTCTTACCACGCGGGCTATCTTCCCTTTTGGGAGCCCCAACAGCGAGG	1002
Sbjct	1307	GGGTGACAGCTTGTGGTCTTACCACGCGGGCTATCTTCCCTTTTGGGAGCCCCAACAGCGAGG	1066
Query	1003	AGAACGACAGATATTGACCTTGTCACACTCTCCAGTCCCCCTGCCCCACAGGAATACA	1362
Sbjct	1367	AGAACGACAGATATTGACCTTGTCACACTCTCCAGTCCCCCTGCCCCACAGGAATACA	1426
Query	1063	TCCAGCTCTGTGTGCTCTCCAGCTCCCGCGCAGGCGCTGTGTGATGGCAAGATCTGTACCG	1122
Sbjct	1427	TCCAGCTCTGTGTGCTCTCCAGCTCCCGCGCAGGCGCTGTGTGATGGCAAGATCTGTACCG	1486
Query	1123	TGACGCGCTGGGCGGACACACAGTACTATGGCGACCGCGGATGCTTCCAGAGAGCTCT	1182

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Sbjct 1487 TGACGGGCTGGGGCAACACGCACTACTATGGCCAAAGCGCGGTACTCCAGGAGGCTC 1546
Query 1183 GAGTCCCCATAATCAGCAATGATGT 1207
Sbjct 1547 GAGTCCCCATAATCAGCAATGATGT 1571

Score = 968 bits (524), Expect = 0.0
Identities = 528/530 (99%), Gaps = 0/530 (0%)
Strand=Plus/Plus

Query 1254 TTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTTC 1313
Sbjct 1573 TTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTTC 1632
Query 1314 TTGTGTGTGAGGACAGCATCTCTCGGAGGCCACGTTGGCGGCTGTGTGGCATTTGTAGT 1373
Sbjct 1633 TTGTGTGTGAGGACAGCATCTCTCGGAGGCCACGTTGGCGGCTGTGTGGCATTTGTAGT 1692
Query 1374 TGGGGCACTGGCTGTGCCCTGGCCGAGGAGGCCAGGCGCTTACACCAAAGTCAGTGACTTC 1433
Sbjct 1693 TGGGGCACTGGCTGTGCCCTGGCCGAGGAGGCCAGGCGCTTACACCAAAGTCAGTGACTTC 1752
Query 1434 CGGGAGTGGATCTTCCAGGCCATAAAGAATCTCACTCCGAAGGCCAGGCGCATGGTGAACCG 1493
Sbjct 1753 CGGGAGTGGATCTTCCAGGCCATAAAGAATCTCACTCCGAAGGCCAGGCGCATGGTGAACCG 1812
Query 1494 CTCGTGACCGGTGGCTTCTGGCTGGCAGGCTCCAGGGCCGAGGATCCCGGTGGTGGG 1553
Sbjct 1813 CTCGTGACCGGTGGCTTCTGGCTGGCAGGCTCCAGGGCCGAGGATCCCGGTGGTGGG 1872
Query 1554 ATCCAGCTGGGCGGAGGAGTGGAGCGTTTTCCTCTTGGGCGCGGTCCACAGGTCCAAAG 1613
Sbjct 1873 ATCCAGCTGGGCGTGAAGTGGAGCGTTTTCCTCTTGGGCGCGGTCCACAGGTCCAAAG 1932
Query 1614 ACACCTTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCAGAGCAC 1673
Sbjct 1933 ACACCTTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCAGAGCAC 1992
Query 1674 CCACACTCACCCCTCTGAGCCCCCATGTAAATATGTTCTGCTGTCTGGAGCTCTGTCTA 1733
Sbjct 1993 CCACACTCACCCCTCTGAGCCCCCATGTAAATATGTTCTGCTGTCTGGAGCTCTGTCTA 2052
Query 1734 GGTGCCCTTGATGATGGGATGCTCTTTAAATAAATAAGATGGTTTGTATT 1783
Sbjct 2053 GGTGCCCTTGATGATGGGATGCTCTTTAAATAAATAAGATGGTTTGTATT 2102

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>emb|CU693028.1| Synthetic construct Homo sapiens gateway clone IMAGE:100019300
5' read HPV mRNA
Length=1222

Score = 1465 bits (793), Expect = 0.0
Identities = 972/1052 (92%), Gaps = 38/1052 (3%)
Strand=Plus/Plus

Query 245 CATGGGCGGAAGGAGGGTGGCCGACTGTGCCATGTGCTCCAGAGCCCAAGGTGGCAGC 304
Sbjct 16 CATGGGCGGAAGGAGGGTGGCCGACTGTGCCATGTGCTCCAGAGCCCAAGGTGGCAGC 75
Query 305 TCTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGCGGCACTCGGGCCATTGT 364
Sbjct 76 TCTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGCGGCACTCGGGCCATTGT 135
Query 365 GGCTGTCTCTCTCAGAGGTGACAGGAGCGGTGTACCCAGTGCAGGTGAGCTCTCGGGA 424
Sbjct 136 GGCTGTCTCTCTCAGAGGTGACAGGAGCGGTGTACCCAGTGCAGGTGAGCTCTCGGGA 195
Query 425 CGCTCGGCTCATGGTCTTTGACAGAGCGGAAGGAGCGTGGCGGCTGCTGTGCTCTCGCG 484
Sbjct 196 CGCTCGGCTCATGGTCTTTGACAGAGCGGAAGGAGCGTGGCGGCTGCTGTGCTCTCGCG 255
Query 485 CTCCAAAGCCAGGTTAGCCGAGCTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGAC 544
Sbjct 256 CTCCAAAGCCAGGTTAGCCGAGCTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGAC 315
Query 545 CCACTCCGAGCTGGAAGTGTGAGACCGGCGGGCCCAATGGCAAGTCGAGCTTCTCTGTGT 604
Sbjct 316 CCACTCCGAGCTGGAAGTGTGAGACCGGCGGGCCCAATGGCAAGTCGAGCTTCTCTGTGT 375
Query 605 GGAAGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTCCGTGTGTGATGTG 664
Sbjct 376 GGAAGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTCCGTGTGTGATGTG 435
Query 665 CCCCAGAGGCGGTTTCTTGGCCGCACTCTGCCAAGACTGTGGCCGAGGAAGTGCACCGT 724
Sbjct 436 CCCCAGAGGCGGTTTCTTGGCCGCACTCTGCCAAGACTGTGGCCGAGGAAGTGCACCGT 495
Query 725 GGAACGCACTGTGGAGAGGCGGAGACACAGCTTGGGCGGCTGGCGTGGCAAGTCAAGCT 784
Sbjct 496 GGAACGCACTGTGGAGAGGCGGAGACACAGCTTGGGCGGCTGGCGTGGCAAGTCAAGCT 555
Query 785 TGCATATGATGGAGCACTCTCTGTGGGGATCCCTGCTCTCCGGGAGCTGGGTGCTGAC 844
Sbjct 556 TGCATATGATGGAGCACTCTCTGTGGGGATCCCTGCTCTCCGGGAGCTGGGTGCTGAC 615
Query 845 AGCCGCCCACTGCTCTCCGAGAGCGGAGCCGGGCTCTGTCCCGATGGCGAGTGTGTGCGG 904

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Sbjct 616 AGCCGCCATTGCTTCCCGAGCCGGAACCGGCTCTGTCCGATGGCGAGTGTTCGCCGG 675  
 Query 905 TGCCGTGGCCCC -AGGCTCTTCCCCACGGTCTGC -AGCTGGGGGTGACGGCTGTGGTCTAC 962  
 Sbjct 676 TGCCGTGGCCCCAG -CTCTTCCCCACGGTCTGC -CTGGGGGGTGGAGCTGTGGTCTAC 733  
 Query 963 CACGGGGG -CTATCTTCCCTTT -CGGACCCCAACAGCGAGGAGAAACAGCAACGA -TATT 1019  
 Sbjct 734 C -CGGGGGGTCT -TCTTCCCTTTTCGG -ACCC -ACCCGCGAGAGAACAGCAACGAATATT 789  
 Query 1020 GGC -CTGGTCCACCTCTCCAGT -CCCCT -GCCCT -CACAGAAATACATCCAGCTG -TGT 1074  
 Sbjct 790 GGCTC -GGTTCACCTTTTCAGTTCCTCCCTGGCTTACCCA -AATAAATCCAGCTGGTGT 847  
 Query 1075 GGCT -CCCAGCT -GCCGGCCAGCCCTGTGGAG -TGGCAAGATCTGT -ACCGTAGCGGG 1130  
 Sbjct 848 GGCTTCCCC -CTTGGCCCGCGGGCCCGGGGGAA TGCCAAGATCTGTATACCGTAGCGGG 906  
 Query 1131 T -GGGG -CAACAGCACTATATG -GCCAACAGGCCG -GGGTACTCCAGGAGGCTCGAG - 1185  
 Sbjct 907 CCGGGGACA -CACCCAGTACTTTGGCG -AACCGGCCCGGGGTATTCCCGAGGTTCTAGG 964  
 Query 1186 TCCCC -ATATCAGCAA -TGA -TGTCTGCAATGGCGCTGACTTCTATGGAAC -CAGATC 1241  
 Sbjct 965 TCTCTATAATAA -CAAAATTAATTTCCAAATGGCGCTTACCTCTCTGTGAATCCGATC 1023  
 Query 1242 A -AGCCCAAGATGTTCTGTGCTGG -CTACCCC 1271  
 Sbjct 1024 TGACCCCAACA -GTATTTTGTCTGTCTACCCC 1054

>dbj|AK095160.1|  Homo sapiens cDNA FLJ37841 fis, clone BR55N2012081, highly similar to SERINE PROTEASE HEPsin (EC 3.4.21.-) Length=2175

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]  
 (Over 10 PubMed links)

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 1404 bits (760), Expect = 0.0  
 Identities = 765/767 (99%), Gaps = 1/767 (0%)  
 Strand=Plus/Plus

Query 695 CCA -AGA CTGTGGCCGACGAAAGCTGCCCGTGGACCGCATGTGTGGAGCCGCGAGACCA 753  
 Sbjct 870 CCA CAGACTGTGGCCGACGAAAGCTGCCCGTGGACCGCATGTGTGGAGCCGCGAGACCA 929  
 Query 754 GCTTGGGCGCGGTGGCCGTGGACGATGAGCTTGGTATGATGAGACCACTCTGTGGGG 813  
 Sbjct 907 GCTTGGGCGCGGTGGCCGTGGACGATGAGCTTGGTATGATGAGACCACTCTGTGGGG 969  
 Query 814 GATCCCTGCTCTCCGGGGACTGGGTGTGACAGCCGCCCACTGCTCTCCGGAGCGGAACC 873  
 Sbjct 990 GATCCCTGCTCTCCGGGGACTGGGTGTGACAGCCGCCCACTGCTCTCCGGAGCGGAACC 1049  
 Query 874 GGGTCTCTGTCCCGATGGCGAGTGTGTGGCCGGTGGCCGTGGCCAGAGCCCTCCCCACGGTC 933  
 Sbjct 1050 GGGTCTCTGTCCCGATGGCGAGTGTGTGGCCGGTGGCCGTGGCCAGAGCCCTCCCCACGGTC 1109  
 Query 934 TGCAGCTGGGGGTGACAGCTGTGGTCTACCAAGGGGGTATCTTCCCTTTGGGAGCCCCA 993  
 Sbjct 1110 TGCAGCTGGGGGTGACAGCTGTGGTCTACCAAGGGGGTATCTTCCCTTTGGGAGCCCCA 1169  
 Query 994 ACAGCGAGAGAAACAGCAACGATATTGGCCCTGGTCCACCTCTCCAGTCCCGGTACTCCA 1053  
 Sbjct 1170 ACAGCGAGAGAAACAGCAACGATATTGGCCCTGGTCCACCTCTCCAGTCCCGGTACTCCA 1229  
 Query 1054 CAGAATACATCCAGCTGTGTGCTCTCCAGCTGCCCGCAGGGCCGTGGTGAATGGCAAGA 1113  
 Sbjct 1230 CAGAATACATCCAGCTGTGTGCTCTCCAGCTGCCCGCAGGGCCGTGGTGAATGGCAAGA 1289  
 Query 1114 TCTGTACCGTGAAGCGGCTGGGGCAACAGCGAGTACTATGGCCAAACAGGCCCGGGTACTCC 1173  
 Sbjct 1290 TCTGTACCGTGAAGCGGCTGGGGCAACAGCGAGTACTATGGCCAAACAGGCCCGGGTACTCC 1349  
 Query 1174 AGAGGCTCGAGTCCCCCAATACAGCAATGATGTCTGCATAGGCGCTGACTTCTATGAA 1233  
 Sbjct 1350 AGAGGCTCGAGTCCCCCAATACAGCAATGATGTCTGCATAGGCGCTGACTTCTATGAA 1409  
 Query 1234 ACCAGATCAGGCCAAGATGTTCTGTGTGGCTACCCCGAGGGTGGCATGTATGCTGCC 1293  
 Sbjct 1410 ACCAGATCAGGCCAAGATGTTCTGTGTGGCTACCCCGAGGGTGGCATGTATGCTGCC 1469  
 Query 1294 AGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGAGACATCTCTGAGACCGGCTGTGGC 1353  
 Sbjct 1470 AGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGAGACATCTCTGAGACCGGCTGTGGC 1529  
 Query 1354 GGCTGTGTGGCATTTGTGAATTTGGGGCACTGGCTGTGGCTTGGCCAGAAAGCAGGCTCT 1413  
 Sbjct 1530 GGCTGTGTGGCATTTGTGAATTTGGGGCACTGGCTGTGGCTTGGCCAGAAAGCAGGCTCT 1589  
 Query 1414 ACACCAAGTCACTGACTCTCCGGGAGTGGATCTTCCAGGCCATAAAG 1460  
 Sbjct 1590 ACACCAAGTCACTGACTCTCCGGGAGTGGATCTTCCAGGCCATAAAG 1636

Score = 601 bits (325), Expect = 4e-168  
 Identities = 325/325 (100%), Gaps = 0/325 (0%)  
 Strand=Plus/Plus

Query 1459 AGAGTCACTCCGAAGCCAGCGCATGGTGAACCAAGCTCTGACCGGTGGCTTCTCGCTGCG 1518  
 Sbjct 1851 AGAGTCACTCCGAAGCCAGCGCATGGTGAACCAAGCTCTGACCGGTGGCTTCTCGCTGCG 1910

Query 1519 CAGGCTCCAGGGCCCGAAGTGAATCCCGGTGGTGGGATCCACGCTGGCCGAGATGGGAC 1578  
 Sbjct 1911 CAGGCTCCAGGGCCCGAAGTGAATCCCGGTGGTGGGATCCACGCTGGCCGAGATGGGAC 1970

Query 1579 GTTTTCTCTCTTGGGCCCCGCTCCACAGGTCCAGGACACCTCCCTCCAGGTTCTCTCT 1638  
 Sbjct 1971 GTTTTCTCTCTTGGGCCCCGCTCCACAGGTCCAGGACACCTCCCTCCAGGTTCTCTCT 2030

Query 1639 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCAACCTCCTGACCCCCAT 1698  
 Sbjct 2031 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCAACCTCCTGACCCCCAT 2090

Query 1699 GTAAATATTGTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758  
 Sbjct 2091 GTAAATATTGTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 2150

Query 1759 TTAAATAATAAAGATGGTTTGAATT 1783  
 Sbjct 2151 TTAAATAATAAAGATGGTTTGAATT 2175

Score = 322 bits (174), Expect = 4e-84  
 Identities = 174/174 (100%), Gaps = 0/174 (0%)  
 Strand=Plus/Plus

Query 363 GTGGCTGTCTCTCTCAGGAGTGAACGAGAGCCCGCTGTACCCAGTGCAGGTCACTCTCG 422  
 Sbjct 159 GTGGCTGTCTCTCTCAGGAGTGAACGAGAGCCCGCTGTACCCAGTGCAGGTCACTCTCG 218

Query 423 GACGCTCGGCTCATGTGCTTTTGAACAAGAGGAGCGTGGCGGCTGCTGTGCTCTCTCG 482  
 Sbjct 219 GACGCTCGGCTCATGTGCTTTTGAACAAGAGGAGCGTGGCGGCTGCTGTGCTCTCTCG 278

Query 483 CGCTCCAAACGCCAGGGGTAGCCCGGACTCAGCTGCAGGAGATGGGCTTCTCTCAG 536  
 Sbjct 279 CGCTCCAAACGCCAGGGGTAGCCCGGACTCAGCTGCAGGAGATGGGCTTCTCTCAG 332

Score = 233 bits (126), Expect = 2e-57  
 Identities = 126/130 (97%), Gaps = 1/130 (0%)  
 Strand=Plus/Plus

Query 533 CAGGGCACTGACCCACTCCGAGCTGGAGCTGCGAAGCGCGGGCCCAATGACAGTCCGG 592  
 Sbjct 400 CAGGGCACTGACCCACTCCGAGCTGGAGCTGCGAAGCGCGGGCCCAATGACAGTCCGG 459

Query 593 CTCTCTCTGTGTGGAAGAGGGAGGCTGCCCCACACCCAGAGGCTGCTGAGGTTCACTCT 652  
 Sbjct 460 CTCTCTCTGTGTGGAAGAGGGAGGCTGCCCCACACCCAGAGGCTGCTGAGGTTCACTCT 519

Query 653 CGTGTG-TGA 661  
 Sbjct 520 CGTGTGTTGA 529


Score = 141 bits (76), Expect = 1e-29  
 Identities = 76/76 (100%), Gaps = 0/76 (0%)  
 Strand=Plus/Plus

Query 288 AGACCCAGAGTGGCAGCTCTCACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGGG 347  
 Sbjct 1 AGACCCAGAGTGGCAGCTCTCACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGGG 60

Query 348 GCATCTGGGCCATTG 363  
 Sbjct 61 GCATCTGGGCCATTG 76

Score = 78.7 bits (42), Expect = 9e-11  
 Identities = 42/42 (100%), Gaps = 0/42 (0%)  
 Strand=Plus/Plus

Query 658 GTGATTGCCCCAGAGGCCGTTTCTTGGCGCCCATCTGCCAAG 699  
 Sbjct 657 GTGATTGCCCCAGAGGCCGTTTCTTGGCGCCCATCTGCCAAG 698

>ref|XM\_001093460.1|  PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 1 (HFN), mRNA  
 Length=2174

GENE ID: 707242 HFN | hepsin (transmembrane protease, serine 1)  
 [Macaca mulatta]

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 1360 bits (736), Expect = 0.0  
 Identities = 757/767 (98%), Gaps = 1/767 (0%)  
 Strand-Plus/Plus

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Query    695   CCA-AGACTGTGGCCGCAAGCAAGCTGCCCGTGGACCGCATCTGTGGAGGCCCGGAGACCA 753
Sbjct    867   CCAAGCACTGTGGCCGCAAGCAAGCTGCCCGTGGACCGCATCTGTGGAGGCCCGGAGACCA 926

Query    754   GCTTGGGCCCGGTGGCCGTGGCAAGTCAAGCTTCGGCTATGATGGAGCAACCTCTGTGGGG 813
Sbjct    927   GCTTGGGCCCGGTGGCCGTGGCAAGTCAAGCTTCGGCTATGATGGAGCAACCTCTGTGGGG 986

Query    814   GATCCCTGCTCTCCCGGGGACAGGTGGTGTGACAGCGGCCCATCTGCTTCCCGAGAGCGGAACC 873
Sbjct    987   GGTCCCTGCTCTCCCGGGGACAGGTGGTGTGACAGCTGCCCCATCTGCTTCCCGAGAGCGGAACC 1046

Query    874   GGCTGCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCTGGCCGAGGCTCTCCCCACGGTC 933
Sbjct    1047   GGCTGCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCTGGCCGAGGCTCTCCCCACGGTC 1106

Query    934   TGCAGCTGGGGGTGCAGGCTGTGGTCTACCAAGCGGGGCTATCTTCCCTTTGGGAGCCCCA 993
Sbjct    1107   TGCAGCTGGGGGTGCAGGCTGTGGTCTACCAAGCGGGGCTATCTTCCCTTTGGGAGCCCCA 1166

Query    994   AAGAGGAGGAGGAGCAAGCAAGCAAGTATGGCCCTGGTCCACCTCTCCAGTCCCTGTCCCTCA 1053
Sbjct    1167   AAGAGGAGGAGGAGCAAGCAAGTATGGCCCTGGTCCACCTCTCCAGTCCCTGTCCCTCA 1226

Query    1054   CAGAAATACATCCAGCCTGTGTGCTCCCAAGCTGCGCGCCAGGCCCTGGTGGATGGCAAGA 1113
Sbjct    1227   CAGAAATACATCCAGCCTGTGTGCTCCCAAGCTGCTGGCCAGGCCCTGGTGGATGGCAAGA 1286

Query    1114   TCTGTACCGTGAAGGGCTGGGGGCAACAGCGAGTACTATGGCCAAAGCGCCGGGGTACTCC 1173
Sbjct    1287   TCTGTACCGTGAAGGGCTGGGGGCAACAGCGAGTACTATGGCCAAAGCGCCGGGGTACTCC 1346

Query    1174   AAGAGGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAA 1233
Sbjct    1347   AAGAGGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAA 1406

Query    1234   ACCAGATCAAGGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGGTGGCATTGAATGCCCTGCC 1293
Sbjct    1407   ACCAGATCAAGGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGGGTGGCATTGAATGCCCTGCC 1466

Query    1294   AGGCGGACAGCGGTGTGCTTCTGTGTGTGAGGACAGCATCTCTCGAGCGCCACGTTGGC 1353
Sbjct    1467   AGGGTGACAGCGGTGTGCTTCTGTGTGTGAGGACAGCATCTCTCGAGCGCCACGTTGGC 1526

Query    1354   GGTGTGTGTGACATTTGTGAGTTGGGACCTGGCTGTGGCTTGGCCAGAGGACAGGCTCT 1413
Sbjct    1527   GGTGTGTGTGACATTTGTGAGTTGGGACCTGGCTGTGGCTTGGCCAGAGGACAGGCTCT 1586

Query    1414   ACACCAAAAGTCACTGATCTCCCGGAGTGGATCTTCCAGGCCATAAAG 1460
Sbjct    1587   ACACCAAAAGTCACTGATCTCCCGGAGTGGATCTTCCAGGCCATAAAG 1633

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Score = 551 bits (298), Expect = 4e-153  
 Identities = 316/325 (97%), Gaps = 0/325 (0%)  
 Strand-Plus/Plus

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Query    1459   AGACTCACTCCGAAAGCCAGCGGACATGGTGAACCAAGCTCTGAACGGTGGCTTCTGCTGGG 1518
Sbjct    1848   AGACTCACTCCGAAAGCCAGCGGACATGGTGAACCAAGCTCTGAACGGTGGCTTCTGCTGGG 1907

Query    1519   CAGCCTCCAGGGGCCGAGGAGTCCCGGTGGTGGGATCCACAGCTGGGCGAGAGATGGGAC 1578
Sbjct    1908   CAGCCTCCAGGGGCCGAGGAGTCCCGGTGGTGGGATCCACAGCTGGGCGAGAGATGGGAC 1967

Query    1579   GTTTTCTTCTTCTGGGCGCGGTCCACAGGTCACAGGACACCTCCCTCCAGGGTCTCTCTCT 1638
Sbjct    1968   ATTTTCTTCTTGGGCGCGGTCCACAGGTCACAGGACACCTCCCTCCAGGGTCTCTCTCTCT 2027

Query    1639   TCCACAGTGGCGGGCCCACTCAGCCCGGAGGACACCCAGCTCAACCTCTGACCCCCAT 1698
Sbjct    2028   TCCACAGTGGCGGGCCCACTCAGCCCGGAGGACACCCAGCTCAACCTCTGACCCCCAT 2087

Query    1699   GTAAATATATGTTCTGCTGTCTGGGATCTCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758
Sbjct    2088   GTAAATATATGTTCTGCTGTCTGGGATCTCTGTCTAGGTGCCCTGATGATGGGATGCTCT 2147

Query    1759   TTAAATTAATAAAGATGGTTTGAATT 1783
Sbjct    2148   TTAAATTAATAAAGATGGTTTGAATT 2172

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Score = 300 bits (162), Expect = 2e-77  
 Identities = 170/174 (97%), Gaps = 0/174 (0%)  
 Strand-Plus/Plus

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Query    363   GTGGCTGTTCTCTCCACAGAGTGAACAGGAGCGCTGTACCCAGTGAGGTCAGCTCAGCTGCG 422
Sbjct    158   GTGGCTGTTCTCTCCACAGAGTGAACAGGAGCGCTGTACCCAGTGAGGTCAGCTCAGCTGCG 217

Query    423   GACGCTCGGCTCATGGTCTTTGACAGAGCGGAGGAGCGTGGCGGCTGCTGTGCTCTCG 482
Sbjct    218   GACGCTCGGCTCATGGTCTTTGACAGAGCGGAGGAGCGTGGCGGCTGCTGTGCTCTCA 277

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Query 483 CGCTCCAA CGCCAGGGTAGCCGGA CTGAGCTGCGAGGAGATGGGCTTCCTCAGG 536
Sbjct 278 CGCTCCAA CACCAAGGGTAGCCGGA CTGAGCTGCGAGGAGATGGGCTTCCTCAGG 331

```

Score = 206 bits (111), Expect = 4e-49  
 Identities = 124/130 (95%), Gaps = 1/130 (0%)  
 Strand=Plus/Plus

```

Query 533 CAGGGCACTGACCCACTCCGAGCTGGAGTGGGACGCGCGGGCCGCAATGGGAGTGGGG 592
Sbjct 399 CAGGGCACTGACCCACTCCGAGTGGAGTGGGACGCGCGGGCCGCAACGGGACGTCAGG 458

```

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Query 593 CTTCTCTCTGTGTGGAGCGAGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC 652
Sbjct 459 CTTCTCTCTGTGTGGAGCGAGGAGGCTGCCACACACCCAGAGGCTGCTGGAGGTCATCTC 518

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```

Query 653 CGTGTG-TGA 661
Sbjct 519 CGTGTGGTGA 528

```

Score = 134 bits (72), Expect = 2e-27  
 Identities = 74/75 (98%), Gaps = 0/75 (0%)  
 Strand=Plus/Plus

```


Query 289 GACCCAGAGGTGGCAGCTCTCACTGCGGGGACCGTGCTACTTCTGACAGCCATCGGGGGGG 348
Sbjct 1 GACCCAGAGGTGGCAGCTCTCACTGCGGGGACCGTGCTACTTCTGACAGCCATCGGGGGGG 60

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Query 349 CATCCTGGGCCATTG 363
Sbjct 61 CATCCTGGGCCATTG 75

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>ref|NM\_00281.3|  Mus musculus hepsin (Hpn), transcript variant 2, mRNA  
 Length=1770

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1303 bits (705), Expect = 0.0  
 Identities = 1343/1644 (81%), Gaps = 71/1644 (4%)  
 Strand=Plus/Plus



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Query 184 ACCCCAGGGTCCCAACCTGGCCCCAGGAGGTGACGAGGGGAATCATTAA CAGAGGCGAGTG 243
Sbjct 148 ACCCCAGGGTTCGCCCCGAGCCCAACAGGTCAACTGGGAATCATTAA CAGAGTTCCTCG 207
Query 244 ACATGGCGCAGAGAGGAGGGTGGCCGGACTG-TGCCATCTGCTCCAGACCCAGGTGGCA 302
Sbjct 208 ACHT-G-GC-GAAGGAGGGTGGCCGGACTGCGAG-CACTGTGCTCCAGACCCAGGTGGCA 263
Query 303 GCTCTCACTGCGGGGACCCCTGTACTTTC-TGACAGCATCGGGGCGGCATCTCGGCGCAT 361
Sbjct 264 GCTCTCATGTGGGTACCCCTGCTG-TTCCTGACAGGCAATGGGGCGGCTCTCGGCGCAT 322
Query 362 TGTGGCTGTCTCTCT-CAGAGGTGACCGAGAGCCGCTGTACCCAGTGCAGCTCAGCTCT- 419
Sbjct 323 TGTGACCATCCTACTGCGAG-AGTGACCAAGGACCACTGTACCAAGTGCAGCTCAG-TCGA 380
Query 421 GCGGACGCTCGGCTCATGGTCTTTGACAGAGCAGGAGGGA-CGTGGCGGCTGTGTGCTCT 478
Sbjct 380 GGGGACTCAGCGCTTGGCGGTGTGTGACAGAGCGA-GGGAACTGGAGGCTCATGTGCTCT 439
Query 479 CTCGCGCTCCAAACGCCAGGATAGCCGGACTCAGCTGCGAGAGGATGGGCTTCTCAGGGG 538
Sbjct 440 CTCACGCTCCAAATGCCAGGGTGGCAGGGCTGCGCTGTGAGAGGATGGGCTTCTCAGGGG 499
Query 539 ACTGACCCACTCCGAGCTGGAAGTGGAGACGCGGGGCGCCATGGCAGCTCGGGCTTCTT 598
Sbjct 500 TCTGGCGCACTCGAGGCTGGATGTGGGCACTGCGGGGCGCCAAACGGCAGCATCGGCTTCTT 559
Query 599 CTGTGTGGACGAGGGGAGG-CTGCCCAACACCCAGAGGCTGCTGGAGGTGATCTCTCGTGT 657
Sbjct 560 TTGGCTGGACGAGGGG-AGACTGCTCTTGGCTCAGAGGTTGCTGGATGTATCTCTGTAT 618
Query 658 GTGATTGCCCCAGAGGCGCTTTCTGGCGGCCACTCTGCCAGACTGTGGCGCGCAGGAGGC 717
Sbjct 619 GTGACTGTCTTAGAGGCGGATTCCTGTGCTGCCACTTGCCAGAGACTGTGGCGCGCAGGAGGC 678
Query 718 TGCCCGTGGACCGCATCTGTGGAGGCGCGGAGCACCGAG-CTTGGGCGGGTGGCGGTGGCAA 776
Sbjct 679 TGCCCGTGGACCGCATTTGTGGGGGGCCAGGACAGCGCTCT-GGGAGGTGGCGGTGGCAG 737
Query 777 GTCAGCCTTCGCTATGATGAGTGG-AGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGGAGTG 835
Sbjct 738 GTCAGCTGCGTATGATGAGTGGAGC-CACCTCTGTGGGGGATCCCTGCTCTCTGGGGAGTG 796
Query 836 GGTGTGACAGCGCCCACTGCTTCCCGGAGCGGAAACCGGGTCCCTGTGCCGATGGCGAGT 895
Sbjct 797 GTGTCTGACTGCTGCACATTCCTTCCAGAGCGGAAACCGGGTCCCTGTCTGCGTGGCGAGT 856
Query 896 GTTTGCGCGGTGCGGTGGGCCCAAG-CTTCTCCCAACGCTGTGCAAGTGAGGCTGAGGCTG 954
Sbjct 857 ATTTGCTGGTGTGTAGCCC-AGACTTCAACCCCATGCTGTGTGCAACTGGGGGTCAGGCTG 915

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ref|NM_017112.1|  Rattus norvegicus hepsin (Hpn), mRNA
emb|X70900.1|RNHEPA  R.norvegicus mRNA for hepsin
Length=1739

GENE ID: 29135 Hpn | hepsin [Rattus norvegicus] (10 or fewer PubMed links)

Score = 1297 bits (702), Expect = 0.0
Identities = 1341/1643 (81%), Gaps = 69/1643 (4%)
Strand=Plus/Plus

Query 184 ACCCCAGGCGTCCCAACCTGACGACGAGGAGTCACGACGAGAAATCATTAACACAGGCGAGTG 243
Sbjct 123 AATGAGTCTGCTCCGCGCCGACGACCTGACCTACCTGGGATCTCTACACAGTCCCTCTG 182

Query 244 ACATGCGCGCAGAGAGGAGGCGTGGCGCGACTGTGGCCATCTGCTGCCAGACCCAAAGTGGCAG 303
Sbjct 183 ACAT-G-GC-AGGAGGGTGGCGCGACTGACGACATGCTGTTCACCAACCAAGTGGGCGAG 239

Query 304 CTCTCACTGTGGGGAGCCCTGCTACTCTCT- TGACAGAGGCATGTGGGGCGCATCTGTGGCCATT 362
Sbjct 240 CTCTCACTGTGGGGAGCCCTGCTGCT- TCTCTGACAGGCATGTGGGGCTGCGTCTCTGGGCAATT 298

Query 363 GTGCGTGTCTCTCT- CAGGAGGTGACACAGGAGGCCGTCTATCCACAGTGCAGGCTCAG-CTCTG 420
Sbjct 299 GTGACCATCTCATCTAG- GGAAGTGCACAGGAGGCCATCTGACCAAGTGCAGCTCAGTCCGGG 357

Query 421 CGAGCGCTGGCTCATGACTCTTTGACACAGAGAGAGGAGGA- GTTGGCGGCTGTCTGTCTCTCC 479
Sbjct 358 -GGACATCTGGCTTTTGTGTCTTTGACACAGAGAGAGGA- GGGAGACATCTGTCTCTCTCTCC 415

Query 480 TCGCGCTCCAAAGCGAGGATGACCGGACTCAGCTGCGACGAGAGATGGGCTTCTCATCGAGCCA 539
Sbjct 416 TCGATCTCCATCCGACAGGATGACAGGGCTCAGGCTGTGGAGAGATGGGCTTCTCATAGGGT 475

Query 540 CTGACCCACTCCAGAGCTGGAGCTGTGGAACTGGCGGGCGCCCAATGCAGCTGTGGGCTTCTCT 599

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Subject	476	CTGGCGCACTCAGACGTGATGTGCAGCCGCCGCGCGCCAAACGCGCATCTCGGCTTCTTC	535
Query	600	TGTGTGGACAGGGGGAGG--CTGCCCAACAACCGAAGGCTGTGGAAGTTCAATCTCGCTGTG	658
Subject	536	TGCTTGACAGAGGGGCG-GGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	594
Query	659	TGATTGCCCAAGGGGCGGCTTTCTTGGCGGCATCTGCGCAAGAAGCTGTGGCCGAGGAAGCT	718
Subject	595	CAGCTGTCTTAGAGGCCGATCTCTTGATGTCACACTGCGCAGACGTGTGGCCGACGAAGAGCT	654
Query	719	GCCCCGTGACCCTCATGTGTGGAGGCCGCGGACACACAGCTTGGGCCGGTGGCCGTGCGAAGT	778
Subject	655	CGCGGTGATGCATTAATGCGGCGCAGACAGCACAGCTGTGAGAACGTGGCCATGGCCAGGTT	714
Query	779	CAGCTTGTGCTATGATGAG--AGGACACTCTGTGTGGAGGATCCCTGTGCTCTCGGGGAATGAG	83
Subject	715	CAGCTTGCGTTATGATGGGAC-C-AACCTCTGTGTGGGAGTCCCTGTGCTCTCGGGGAATGAG	773
Query	838	TGCTGACAGCGCCCACTGTCTCCCGAGCGAAACCGGCTCTGTCCGATGCGAGTGTGT	897
Subject	774	TACTGACCGTGCACACTGCTTTCACAGAGGAACCGGGTCTGTCTCGTGGCGATAT	833
Query	898	TTGCGGTGTGCTGTAGGCC--CGCTCTCCCACGATC-TGTGACCTTGGGGTGTCAAGCTGT	955
Subject	834	TTCTTGGTGCTGTAGGCC-AGCCACTCACTCATGCG-CGTGACCTTGGGGTGTCAAGCTGT	951
Query	956	GGTCTACAGCGGGGGCTATCTTCCCTTTTCGAGACCCCAAC-AGCGAGAGGAACGACAGCS	1014
Subject	892	GATCTATCATGPGGGGGCTATCTTCCCTTTTCGAGACCCCTA-CTATCGAGAAACGACAAATG	950
Query	1015	ATAATGCCCTTGTCCACTCTCCAG-TCCCCTGCCCTCAGAGAAATATCCAGCCCTGTG	1073
Subject	951	AATCTTGCCCTTGTCCACTCTCAGCTCCC-TGCGCTCTCAGAGAAATATCCAGCCCGGTT	1009
Query	1074	TGCTCCCAAGCTGCGCGCGCCAGCTTGGTGAATGAGCAAGTCTGTATACGTACGAGGCTGTG	1133
Subject	1020	TGCTCTCCCTGCTGCGGGACAGGCCCTTGTGAGCGCAAGGCTCTATCAAGTGAACGCGCTG	1069
Query	1134	GGCAACACAGCATATAATGCGCAACAGCGCGGGGTATCTCAGAGAAGCTCGAGTCCCCATA	1129
Subject	1070	GGTAAACACAGTGTATATGCGCAACAGAGCTGTGGTGTCTCAGAGAGGCCCGGGTCCCGATC	1123
Query	1194	ATCGAAGATGATGTCTGACATAGCGCTGATCTCTATAGAAAACAGATCAAGCGCCAAAGTGT	1253
Subject	1130	ATAGAGAGAGAGGTTTGACACAGCCCGGATCTTACAGGGATCTAGTATAGAAACAGAGTGT	1189
Query	1254	TTCTGTGCTGGTACCCCGAGGGTGGCATTTGATGCTGCGCAGGGGACAGCGGTGTGTC-	1312
Subject	1190	TTCTGTGCTGGTACCCCGAGGGTGGCATTTGATGCTGCGCAGGGGACAGCGGGTGTGTC-	1248
Query	1313	CTTTGTGTGTAGGAACGACATCTCTCGAG--GGCCAGCTTGGCGGCTGTGTGTGCATTTGGA	1371
Subject	1249	CTTTGTGTGTAGGAACGACATCTCTCGAATCAGAGTGTGCGCTCTGTGCGCATTTGTAA	1307
Query	1372	GTTGGGGCATGTGCTGTAGCTCGCCAGGACGAGGAGCTGTGACCAAAGTCAAGTGAAT	1361
Subject	1308	GTCTGGGATCGGGTGTGCTTGTGGCGCGGACAGGAGAGCTGTGACCAAAGTCAAGTGAAT	1367
Query	1432	TCCGGAGAGTGTCTTCCAGGCCATAAAGATCACTACCGAAGCAGCGGCTAGGTGAACCC	1491
Subject	1368	TCCGGAGAGTGTGATCTTCCAGGCCATAAAGATCACTACCGAAGCAGCGGCTAGGTGAATCC	1427
Query	1492	AGCCCTGACCGG-G--TG---GCTT-GC-GC--TGCGC-AGCCCTCAGGGGCCAGAG--G-	1537
Subject	1428	AGCCCTGACCCCGCTCATGCGCTGCTCGCGCTGCTCCAGCTCAGGGGCTCAGAGTTGG	1487
Query	1538	T--GAT--C-CGGT-G--GTGGAG---TCCAAGCTTGGGCG-AGATGTGAAGCTTTTT	1584
Subject	1488	TTTGTTGCTTCCAGCGCCAGCTTGCAGGCTCCACATCGAGCTCTCAC-ATGGAAGCTTTTT	1546
Query	1585	CTTCTTGGGCGCGCCACAGTCCAGGACCACTCCCTCCGCAAGGCTCTCTCTCTCCACA	1646
Subject	1547	CTGCTCGAGTCCAGTCCATGAGTCCAGGAGATGC--TGGGTCAAAGAGCTCTCTCTCCACA	1604
Query	1645	GTGCGGGGCCCATCTCAGCCCC-GAGACACCCCAAGCTCACTCTCTGACCCCCCATGTAA	1703
Subject	1605	GTGCGGGGCCCATCTCAGCCCC-GCATTGG-CTCTCACTCTCC-ACCC-ATGTAA	1660
Query	1704	TATGTGTTCTGCTGTCTGAGAA-CTCTGTTATGGTGCACCGCTGATGTG-AGATGCTCTTT	1760
Subject	1661	TATTACTCTGTCC-TCGTGGGGGTCTGTGTGAGGGCGCCCT--TG-TGCGATGCTCTTT	1716
Query	1717	AAAAATAAAGATGGTTTGTATT	1783
Subject	1717	AAAAATAAAGATGGTTTGTATT	1739

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>gb|AF030065.1|AF030065  Mus musculus serine protease hepsin mRNA, complete cds
Length=1781
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GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1280 bits (693), Expect = 0.0  
Identities = 1341/1646 (81%), Gaps = 75/1646 (4%)  
Strand=Plus/Plus

Query 184 ACCCCAGGGTCCCACCCCTGGCCCAGGAGGTCAGCCAGGGAATCATTAAACAAGAGGCAGTG 243

Sbjct 143 ACCCCAGGGTTTCGGCCCCAGCCCCAACAGGTCACCTGGGAATCATTAAACAGAGTTCCTCTG 202

Query 244 ACATGGCCGACAGAGAGAGGTGGCCGAGCTG - TGCCATGCTGCTCCAGACCCAGAGTGGCA 302

Sbjct 203 ACAT - G - GC - GAGGAGGGGTGGCCGAGCTGCA - CATGCTGCTCCAGACCCAGAGTGGCA 258

Query 303 GCTCTCACTGCGGGGACCCCTGCTACTTC - TGACAGCCATCGGGGGCGGCACTCTCGGCCAT 361

Sbjct 259 GCTCTCATTTGCTGGTACCCCTGCTG - TTCTTGACAGGCAATTGGGGCCGCTCTCTCGGCCAT 317

Query 362 TTGTGGCTGTCTCCT - CAGGAGTGACAGGAGGCCGTGTACCCAGTGCAGGTCACTCT - 419

Sbjct 318 TTGTGACCATCTACTGACAG - AGTGACAGGAGGCCATGTGTACCAAGTGCAGCTCAG - TCCA 375

Query 420 GCGGACGCTCGGCT - - CATGGTCTTGACAGAGCGGAAGGG - ACCTGGCGGCTGCTGTGTC 476

Sbjct 376 GGGGACTCACGACTTGCA - G - TTGTGGACAGAGCGGA - GGGTACGTGGAGGCTACTGTGTC 432

Query 477 TCTCTCGGCTCCAGCCGAGGGTAGCCGAGCTCAGCTGCGAGGAGATGGGCTTCTCTCAGG 536

Sbjct 433 TCTCTCAGCTCCAAAGCCAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCTCAGG 492

Query 593 GCACTGACCCCACTCCGAGCTGGACGTTGGAGCGCGGGCGCCAAATGGCACTCGGGCTTC 596

Sbjct 493 GCTCTGGCGCACTCCGAGCTGGATGTGGCGCACTGGCGGCGCCAAACGGCACTCGGGCTTC 552

Query 597 TTCTGTGTGGACAGGGGAGG - CTGGCCCAACCCAGAGGCTGCTGGAGGTCATCTCCGTT 655

Sbjct 553 TTTTGTGTGGACAGGGG - GGA - CTGCTCTGGCTCAGAGGTGCTGTGATGTATCTCTGT 611

Query 656 GTGTGATTGGCCCAAGGGCCGTTTCTTGGCCGACATCTGCGAAGACTGTGGCCGCGAGAA 715

Sbjct 612 ATGTGACTGTCTTAGAGGCCGATTTCTGACTGCTGCCACCTGCCAAGACTGTGGCCGCGAGAA 671

Query 716 GCTGCCCGTGGACCGCACTGTTGGAGGGCCGAGACACCAAG - CTTGGGCGCGGTGGCCGTGGC 774

Sbjct 672 GCTGCCCGTGGACCGCACTGTGTGGGGGGCCAGGACAGCAGTCT - GGGAGAGGTGGCCGTGGC 730

Query 775 AAGTCAGCCCTTCCTATGATGG - AGCACTCTGTGGGGGATCCCTGCTCTCGGGGAC 833

Sbjct 731 AAGTCAGCCCTGCTATGATGGGACC - CACCTCTGTGGGGGTCCCTGCTCTGGGGAC 789

Query 834 TGGGTGTGACAGCGCCCACTGCTTCCCGGAGCGGAACCGGGTCTCTGTCCCGATGGCGA 893

Sbjct 794 TGGGTGTGACTGCTGACCATTTCTTCCAGAGCGGAACCGGGTCTCTGTCTGGTGGCGA 849

Query 890 GTGTTTTCGCGGTGCGGTGGCCAGG - CCTCTCCCAAGCTCTGACGCTGGGGGTGCGAGGC 952

Sbjct 850 GTATTTCGTGTGCTGAGCCC - GGA - CTTACCCCATGCTGTGCACTGGGGGTTCAGGC 908

Query 953 TTGTGGTCTACACCGGGGCTATCTTCCCTTTTCGGGACCCCAAC - AGCGAGGAGGAACAGCA 1011

Sbjct 909 TTGTGATCTATCATGGGGGCTACCTTCCCTTTTCGAGACCCCTA - CTATTGACGGAACAGCA 967

Query 1012 ACGATATTGCCCTGGTTCACCTCTCAG - TCCCTGTCGCCCTCAGAGATACATCTCCAGCCT 1070

Sbjct 968 ATGACATTTGCTTGGTTCACCTCTCTGCTCC - TGCTCTCAGAGATACATCTCCAGCCTA 1026

Query 1071 GTGTGCCCTCCAGCTGCGCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGAACGGGC 1130

Sbjct 1027 GTGTGCTCCCTGCTGCGGAGCAGGCCCTGGTGGATGGCAAGTCTGTATCTGTGACCGGC 1086

Query 1131 TGGGGCAACACGCACTATATGGCCCAAGGCCGGGATATCCAGAGAGGCTCGAGTCCCC 1190

Sbjct 1087 TGGGGTAAACACAGTCTATATGGCCCAAGGCTATGTGCTCCAGAGAGGCCGGGTTCCT 1146

Query 1191 ATTAATCAGCAATGATGTCTCTCAATGGCGCTGACTTCTATGAGAAACAGATCAAGCCCAAG 1250

Sbjct 1147 ATCTAAGCAACAGAGTTTGCAACAGCCCGCACTTCTACGGAATCAGATCAAGCCCAAG 1206

Query 1251 ATGTTCCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCTTCCAGGGCGACAGCGGTGGT 1310

Sbjct 1207 ATGTTCCTGTGCTGGCTATCCTGAGGGTGGCATTGATGCTTCCAGGGCGACAGCTGGAAGC 1266

Query 1311 CCCCTTGTGTGTGAGGACAGCATCTCTGGAGCGCAAGTTGGCGGCTGTGTGGCTATTGTG 1370

Sbjct 1267 CCCCTTGTGTGTGAGGACAGCATCTCTGGGACATCAAGGTGGCGGCTATGTGTGATTTGTA 1326

Query 1371 AGTTTGGGGCACTGGGCTGTGCTCCGCCCCAGAGGCCAGGCGTCTACACCAAGTCAAGTGAAC 1430

Sbjct 1327 AGCTTGGGGTACCGGCTGTGCTTTGGCCCGGAGGCCAGGAGTGTACACCAAGTCACTGAC 1386

Query 1431 TTCCGGGAGTGGATCTTCCAGGCCATAAGACTCACTCCGAGGCCAGCGCATGGTGAACC 1490

Sbjct 1387 TTCCGGGAGTGGATCTTCCAGGCCATAAGACTCACTCCGAGGCCAGTGGCTATGGTGAACC 1446

Query 1491 CAGCTCTGA - CCGG - TGG - CT - - T - CTC - G - - CTGCG - AGCCTCCAGGCGCCGAG - 1536

Sbjct 1447 CAGCCCTGAACCCGCGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506

Query 1537 G - T - GAT - C - CC - G - - - - GTGGTGGGATCCAGCTGGGGCG - AGGATGGGACGTTT 1582

Sbjct 1507 GGTCTGTGGCTCCAGGCCCACTGTGATGGCTCCACACTTGGGCTTAC - ATGAGATGGTT 1565


Query 1583 TTCTCTTGGGCCCCGCTCCACAGGTCCAGGACACCCCTCCCTCCAGGTCCTCTCTTCCA 1642

Sbjct 1566 TCTGCTCAGATGCCAGTCCAGGCTCCAGGATGC - - TGGATCAAGGACTCTCTCTTCCA 1623

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Query 1643  CAGTGGCGGGCCCACTCAGCCCC-GAGACCACCAACCTCACCCCTCTGACCCCACTGTA 1701
             |||||
Sbjct 1624  CAGTGGCGGGCCCACTCAATCCAGGG-CCATTGG-CTTCACCCCTCCC-ACCCC-ATGTA 1679
Query 1702  AATATTGTCTTG-CGTCTCGGAGTC-CGTGCTAGGT-GCCCTGATGATGG-GATGCTC 1757
             |||||
Sbjct 1680  AATATTACTCTGTCC-TCTGGGGGGCGCT--CTAGGGAGCCCCCT--TG-TGCAGATGCTC 1733
Query 1758  TTTAAATAATAAGATGGTTTGTATT 1783
Sbjct 1734  TTTAAATAATAAGTGGTTTGTATT 1759

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>ref|NM\_001110252.1|  Mus musculus hepsin (Hpn), transcript variant 1, mRNA  
Length=1830

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1245 bits (674), Expect = 0.0  
Identities = 1282/1569 (81%), Gaps = 68/1569 (4%)  
Strand=Plus/Plus

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Query 259  AGGGTGGCGGGCTG-TGCCATGTCTCCAGACCCAGGTGGCAGCTCTCATGCGGGG 317
             |||||
Sbjct 280  AGGGTGGCGGGCTGCGA-CATGTCTCTCCAGACCCAGGTGGCAGCTCTCATATGTGGT 338
Query 318  ACCCTGCTACTTC-TGACGACCTCGGGGCGCATCTGGGCAATTGTAGCTTCTCTCT 376
             |||||
Sbjct 339  ACCCTGCTG-TTCTGACAGGCATTGGGGCGCGTCTCTGGGCAATTGTAGCTCTCTCT 397
Query 377  -CAGGATGTGACAGGAGCGCGCTGTATCCCAAGTCAGGTCAGCTCT-GCGGAGCGTCGGCTC 434
             |||||
Sbjct 398  CGAG-AATGACACGAGAGCCACTGTATCCCAAGTCAGGTCAG-TCCAGGGAGCTCACGGCTT 455
Query 435  ATGGCTCTTGAACAGACGGAGGGAG-CGTGGCGGCTGCTGTGCTCTCTCGCTCCAAAGC 493
             |||||
Sbjct 456  GCGGTCTTGAACAGACGGA-GGGAAAGTGGAGGCTACTGTGTCTCTCACGCTCCAAATGC 514
Query 494  CAGGGTAGCGGAGCTCAGCTGCGAGGAGATGGGCTTCCCTCAGGGCAGTCAGCCCATCCGA 553
             |||||
Sbjct 515  CAGGGTAGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCAGGGCTCTGGGCGACTCGGA 574
Query 554  GCTGAGCGTGCAGAACGGCGGGGCCAATGGCAGTCGGGGCTTCTCTGTGTGAGACAGGG 613
             |||||
Sbjct 575  GCTGAGTGTGCGCATGCGGGGCGACAGGCGCATCTGGGCTTCTCTGTGTGAGACAGGG 634
Query 614  GAGG-CTGCCCCACACCGAGAGGTGCTGGAGGTCACTCTCGTGTGTGATGTCCCCAGAG 672
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Sbjct 635  C-GGATGCTCTTGGCTCAGAGGTGCTGGATGTATCATCTCTGTATGTGATCTGTCTTAGAG 693
Query 673  GCGGTTTCTTGGCGGCACTTCCCAAGATCTGTGGCCGACAGGAAGTCCCGGTGTGACCGCA 732
             |||||
Sbjct 694  GCGGATCTCTGATCTGCACTCTGCCAAGATCTGTGGCCGACAGGAAGTCCCGGTGTGACCGCA 753
Query 733  TCGTGGAGGCGGGGACACAG-GCTGGGCGGGTGGCGGTGGCAAGTCAAGCTCTGCTAT 791
             |||||
Sbjct 754  TTGTGGGGGGCCAGGACAGCATCTT-GGGAGGTGGCGGTGGCAGGTCAAGCTCTGCGTTAT 812
Query 792  GATGG-AGCACACCTCTGTGGGGGATCCCTGCTCTCTCCGGGGACTGGGTGCTGACAGCGCG 850
             |||||
Sbjct 813  GATGGGAGC-CACCTCTGTGGGGGGTCCCTGTCTCTGGGGACTGGGTGCTGATCTGTCTG 871
Query 851  CCACTGCTTCCCGAGAGCGAACCGGGTCTGTCCCGATGGCGAGTGTGTTCGGGTGGCGGT 910
             |||||
Sbjct 872  ACHTGTCTTTCAGAGAGCGGAGCCGGGTCTGTCTCGGTGGCGAGATATTTGTGTGTGTGT 931
Query 931  GGCCCAAG-CCTCTCCCCACGCTCTGAGCTGGGGGTGCAAGCTGTGGTCTACACAGCGGG 969
             |||||
Sbjct 932  AGCCCC-GGACCTTCAACCCATGCTGTGCACTGGGGGTTCAAGCTGTGATCTATCTATGGGG 990
Query 970  GCTATCTTCTCCCTTTTGGGAGACCCCAAC-AGCGAGAGAGACAGCAAGATTTTTCGGGTGCT 1028
             |||||
Sbjct 991  GTATCTTCTCCCTTTTGGAGACCTCA-CTATCGAGAGAGACAGCAAGATTTTGTGTGTGT 1049
Query 1029  CACCTCTCCAG-TCCCTGTCCCTTACAGAAATACATCCAGCGCTGTGTGTCTCCACAGTGC 1087
             |||||
Sbjct 1050  CACCTCTCTAGCTCCC-TGCCTCTACAGAAATCATCAGCAGATGTGTCTCTCCACAGTGC 1108
Query 1088  CGGCCAGGCGCTGTGTGAGTGGCAAGATCTGTACCGTGAACGGTGGGGCAACAGCAGTA 1147
             |||||
Sbjct 1109  GGGACAGGCGCTGTGTGAGTGGCAAGTCTGTATGTGACCGGTGGGGTAACACAGATTT 1168
Query 1148  CTATGGCCACAGGCGCGGGTATCTCCAGAGGCTCGAGTCCCAATACATGATGATGT 1207
             |||||
Sbjct 1169  CTATGGCCACAGGCTATGTGTCTCCAGAGGCGCGCGGTCTCCATCATAGCAACAGAGT 1228
Query 1208  CTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTCTGTGTCTGGCTA 1267
             |||||
Sbjct 1229  TGTCAACAGGCCCGGACTTCTATCGGAATCAGATCAAGCCCAAGATGTCTGTGTCTGGCTA 1287
Query 1268  CCCCAGAGGGTGGCAATGATGCTCTCCAGGCGGACAGCGGTGTGCTCTTGTGTGTGAAGA 1327
             |||||
Sbjct 1289  TCCTGAGGGTGGCAATGATGCTGTGCGTGCAGGGGCGACAGTGGAGGCCCTCTTGTGTGTGAAGA 1348
Query 1328  CAGCATCTCTCGAGCGCCAGTGGCGGCTGTGTGGCATTTGTGAGTTGGGGCACTGGCTG 1387

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Sbjct 1349 CAGCATCTCTGGGACATCAAGGTGGCGGCTATGTGGCATTTGTAAGCTGGGGTACGGGCTG 1408
Query 1388 TGCCCTGGCCCAAGAGCCAGAGCGTCTACACAAAGTCAGTGACTTCGGGAGGTGGATCTT 1447
Sbjct 1409 TGCTTTGGATCGGAGGCCAGAGATGTTCACAGAGTCACTGACTTCGCGGAGTGGATCTT 1468
Query 1448 CCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGAACCAAGCTCTGA-CCGG--T 1504
Sbjct 1469 CAGAGCCATAAAGACTCACTCCGAAGCCAGTGGCATGTGACTCAAGCCGTATCCCGCT 1528
Query 1505 GG-CT---T-CTC-G-CTGCGC-AGCCTCCAGGGCCCGAG--G-T--GAT--C-CC-G- 1545
Sbjct 1529 CATCTCGTCTGCTCCGCTGCTCATAGCATCCAGAGTCAGAGTTGGTCTGGTGGCTCCAG 1588
Query 1546 -----GTGGTGGGATCCACGCTGGGCGG-AGGATGGGAGCTTTCTCTCTTGGGCCCGGT 1599
Sbjct 1589 CCCACGTGGTAGGCTCCACACTGGGCTCAC-ATGGAAATGTTCTCTGCTCAGATCCAGT 1647
Query 1600 CCACAGGTCCCAAGGACACCCCTCCCTCAGGGGTCTCTCTTCCACAGTGGCGGGCCCACTC 1659
Sbjct 1648 CCACGGGTCCCAAGGATGC--TGGATCCAAAGGACTTCTCTTCCACAGTGGCGGGCCCACTC 1705
Query 1660 AGCCCC-GAGACCCACCCACCTCACCTCTGACCCCCCATGTAAATATTGTTCTG-CTGT 1717
Sbjct 1706 AATCCCAAGG-CCATTGG-CTCACCTTCCC-ACCCC-ATGTAAATATTACTCTGTCC-T 1760
Query 1718 CTGGGACTC-CTGTCTAGGT-GCCCCGTGATGATGG-GATGCTCTTTAAATAATAAAGATG 1774
Sbjct 1761 CTGGGGGGCGCT--CTAGGAGGCCCTC--TG-TGCAGATGCTCTTTAAATAATAAAGGTG 1815
Query 1775 GTTTTGATT 1783
Sbjct 1816 GTTTTGATT 1824

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**gbl|C138809.1|** Mus musculus hepsin, mRNA (cDNA clone MGC:170436 IMAGE:8861831), complete cds  
Length=1505

Score = 1240 bits (671), Expect = 0.0  
Identities = 1075/1271 (84%), Gaps = 23/1271 (1%)  
Strand=Plus/Plus

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Query 259 AGGGTGGCCGGAAGT-GGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCATGCGGG 317
Sbjct 160 AGGGTGGCCGGAAGTCAAG-CATGCTGCTCCAGACCCAAGGTGGCAGCTCTCATGCGGG 218
Query 318 ACCCTGCTACTTC-TGACAGCCATCGGGGCGCATCTGGCCATTGGCTGTTCTCTCT 376
Sbjct 219 ACCCTGCTG-TTCTGACAGGCAATGGGGCCGCTCTGGGCCATTGTGACCATCTACT 277
Query 377 -CAGGAGTGACCAAGAGCGCGCTGTACCCAGTGCAGGTCAAGCTCT-GCGGAGCTGGCTC 434
Sbjct 278 CGAG-AGTGAACAGAGGCACTGTACCAAGTGCAGGTCAAG-TCCAGGGGACTCAAGGCTT 335
Query 435 ATGGTCTTTGACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTCTCGCGCTCCAAAGC 493
Sbjct 336 GCGGTGTTTGAACAAGACGGA-GGAAATGGGAAGGTAAGTGTCTCTCAAGCTCCAAAGC 394
Query 494 CAGGGTAGCCGGAATCAAGCTGCGAGGAGATGGCTTCTCCAGGGCACTGAACCCATCCGA 553
Sbjct 395 CAGGGTAGCAAGGCTCGCGCTGTGAGGAGATGGCTTTCTCAAGGCTTGCGGCACTCGGA 454
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Sbjct 455 GCTGGATGTGCGCACTGCGGGGCCAAGCGGCAATCGGGCTCTTTTTCGCTGGAAGAGGG 514
Query 614 GAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTCCGTGTGTGATGTGCCCAAG 672
Sbjct 515 C-GGACTGCCCTTGGCTCAGAGGTTGCTGGATGTCACTCTGTATGTGAAGTCTCTTAGAG 573
Query 673 GCCGTTTCTTTGGCCGCACTTGCACAGACTGTGGCCGCAAGGAGCTGCCCGTGGAGCGCA 732
Sbjct 574 GCCGATTCTGACTGCACTGCAAGCTGCAAGACTGTGGCCGCAAGGAGCTGCCCGTGGAGCGCA 633
Query 733 TGTGGGAGGCGGGAACCAAG-CTTGGGCGGTTGGCGGTGGGAGAGTCAAGCTCTGCTAT 791
Sbjct 634 TTGTGGGGGGCCAGGACAGAGTCT-GGGAAAGTTGGCGGTGGGAGGTCAGGCTGCGTAT 692
Query 792 GATGG-AGCAACCTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGGGTGCTACAGCCGCG 850
Sbjct 693 GATGGGAGC-CACCTCTGTGGGGGGTCCCTGCTGCTCTGGGAGCTGGGTGCTGACTGCTGC 751
Query 851 CCACCTGCTCCGAGAGCGGAACCGGCTCCGTGCTCCGAGTGGGAGATGTTTTCGCGCTGCT 910
Sbjct 752 ACATTGCTTTCCAGAGCGGAACCGGCTCCGTGCTCCGAGTGGGAGATGTTTTCGCGCTGCT 811
Query 911 GAGCCAGG-CCTCTTCCCAAGCGCTTGCAGCTGGGGGTGCAAGCTGTGGTCTACACAGCGGG 969
Sbjct 812 AGGCC-GGACTCAACCCCATGCTGTGACATGGGGGTTCAAGGCTGTGATCATATAGGG 870
Query 970 GCTATCTTCCCTTTTGGGAGCCCAAC-AGCGAGGAGAACAGCAAGATATGTCCTGGTC 1028
Sbjct 871 GCTACTTTCCTTTTGGGAGCCCACT-CTATGAGAGAAACAGCATGACATGCTTGTGCT 929
Query 1029 CACTCTCCAG-TCCCTTGGCTCTACAGATACATCCAGCTGTGGTGGCTCCAGCTGC 1087
Sbjct 930 CACCTCTTAGCTCCC-TGCCCTCTACAGATACATCCAGCAGTGTGTCTCCGCTGCTGC 988

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Query 1088 CCGCAGAGCCCTGGTGGATGGCAGATCTGTACCGTGACCGGCTGGGGCAACACGAGTA 1147
Sbjct 989 GGGACAGAGCCCTGGTGGATGGCAGATCTGTACCGTGACCGGCTGGGGTAAACACAGTT 1048
Query 1148 CTATGGCCAAACAGGCGGGGTACTCCAGGAGGCTCGAGTCCCAATACGCAATGATGT 1207
Sbjct 1049 CTATGGCCAAACAGGCTATGGTGTCCAGAGGGCCGGGTTCCCATCATGACACAGAGT 1108
Query 1208 TGCCTATGGCGTGAATCTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTA 1267
Sbjct 1109 TTGTAACAGCCCGGACTCTTACCGGATCGAGTCAAGCCCAAGATGTTCTGTGCTGGCTA 1168
Query 1268 CCCCAGAGGTGGCATTTGATGCTGCGCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGA 1327
Sbjct 1169 TCCTAGAGGGTGGCATTTGATGCTGCGCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGA 1228
Query 1328 CAGCATCTCTCGAAGCCCAAGTTGGCGGCTGTGTGGCAITGTGAGTTGGGGCACTGGCTG 1387
Sbjct 1229 CAGCATCTCTGGGACATCAAGTGGCGGCTATGTGGCAITGTGAGTTGGGGCACTGGGGCTG 1288
Query 1388 TGCCCTGGCCCAAGAGCCAGAGGTCTACCAAAAGTCAGTGACTTCGCGGAGTGGATCTCT 1447
Sbjct 1289 TGCTTTGGCCCGGAGGCCAGGAGTGTACACAAAGTCACTGACTTCGCGGAGTGGATCTCT 1348
Query 1448 CCAGGCCATAAAGACTCACTCCGAGGCCAGCGGCTGTGTAAGCCAGCTCTGA-CCGGTGG 1506
Sbjct 1349 CAAAGCCATAAAGACTCACTCCGAGGCCAGTGGCTGTGTAAGCCAGCTCTGA-CCGGCTCT 1408
Query 1507 CTTCTCGCTGC 1517
Sbjct 1409 CATCTCGCTGC 1419

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>dbj|AK156553.1|  Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830029I12 product:hepsin, full insert sequence  
length=1745

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1240 bits (671), Expect = 0.0  
Identities = 1282/1570 (81%), Gaps = 70/1570 (4%)  
Strand=Plus/Plus

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Query 259 AAGGTGGCCGGAATG-TGCCATGCTGCTCCAGACCCAAAGTGGCAGCTCTCACTCGGGG 317
Sbjct 199 AAGGTGGCCGGAATGCAAG-CATGCTGCTCCAGACCCAAAGTGGCAGCTCTCACTGTGGGT 253
Query 318 ACCCTGCTACTTC-TGACAGCCATCGGGGCGGCATCTCGGACATTGTGGCTGTCTCTCT 376
Sbjct 254 ACCCTGCTG-TTCTGACAGGACTTGGGGCGGCTCTCGGACATTGTGACCACTCTACT 312
Query 377 -CAGGATGACCAAGAGCGCCGCTGTACCCAGTGCAAG-TCACTCT-CCGGAAGCTGGGCT 433
Sbjct 313 GCAG-AGTGACCAAGAGCCACTGTACCAAGTGC-GGCTCAG-TCCAGGGAGCTACAGGCT 369
Query 434 CATGGTCTTTGACAGAGAGAGAGGA-CGTGGCGGCTGCTGTGCTCTCGCGCTCAACAG 492
Sbjct 370 TGCCTGTGTTGACAGAGAGAG-AGGAACGTGGAAGCTACTGTGCTCTCTCAAGCTCAAGT 428
Query 493 CCAGGGTAGCCGGAATCAAGCTGCGAGGAGATGGGCTTCTCCAGGCACTGACCCCACTCCG 552
Sbjct 429 CCAGGGTGGCAAGGCTCGGCTGTGAGGAGATGGGCTTCTCCAGGCACTTGGCACTCGG 488
Query 553 AGGTGGACGTGAGAGAGCGCGGGCGCCAAAGGCACTCGGAGCTTCTCTGTGTGAGAGAGG 612
Sbjct 489 AGCTGGATGTGCGCACTCGGCGCCCAAGGCACTCGGAGCTTCTTTGCTGTGAGAGAGG 548
Query 613 GGAGG-CTGCCCCACACCCAGAGGCTGTGGAGGTGATCTCCGTGTGTGATTGCCCCAG 671
Sbjct 549 GC-GGACTGCTCTGGCTCAGAGGTTGCTGGATGTCACTCTGTATGTGACTGCTCAG 607
Query 672 GCGCGTTCTTGGCGCCGCACTGCGCAGAGCTGTGGCCGCAAGAGAGCTGCGCGTGAACGCG 731
Sbjct 608 GCGCGATTCTCTGACTGCCCACTGCCAAGAGCTGTGGCCGCAAGAGAGCTGCGCGTGAACGCG 667
Query 732 ATCGTGGGAGGCGGGAACACAG-CTTGGGCGGCTGGCGGTGGCAAGTCAAGCTTGTGCTA 790
Sbjct 668 ATTGTGGGGGCAAGAGACAGCATCT-GGGAAGTGGCGGTGGCAGTCAAGCTTGTGCTA 726
Query 791 TGATGG-AGCAACCTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAACAGCG 849
Sbjct 727 TGATGGGA-CTCACTCTGTGGGGGATCCCTGCTCTGCGGAGCTGGGTGCTGAACAGCG 785
Query 850 CCCACTGCTTCCCGGAGCGAGAACCGGGTCTGTCCCGATGGCGAGTGTGTTGCGGGTCCG 909
Sbjct 786 CACATTGCTTCCAGAGCGAGAACCGGGTCTGTCTCGGTGGCGAGTATTGCTGTGCTG 845
Query 910 TGCCCCAGG-CCTCTCCCCAGGCTGCAAGCTGGGGGTGCAAGGCTGTGCTTACCAACGCG 968
Sbjct 846 TAGCCC-GGAGCTCAACCCATGCTGTGCAACTGGGGGTTCAGGCTGTGATCTATCAAGG 904
Query 969 GGCTATCTTCCCTTTCCGGGACCCCAAC-AGCGAGGAGAGACAGCAAGATATGCTGCCCTGGT 1027
Sbjct 905 GGCATCTTCCCTTTCCGGGACCCCAAC-CTATCGAGAGAGAGACAGCAAGATGCTGCCCTGGT 963
Query 1028 CCACCTCTCCAG-TCCCTCGCCCTCCAGAAATACATCCAGCTGTGTGCTCCAGCTG 1086

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Sbjct 964      CCACCTCTCTAGCTCCC - TGCCCTCTCAGGAATACATCCAGCCAGTGTGTCTCCCTGCTG 1022
Query 1087      CCGCCCAAGCCCTGTGATGCGATGCAAGATCTGTACCGTGAAGCGGCTGCGGCAACAGCAGT 1146
Sbjct 1023      CCGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCCTGGGGTATACACACAGT 1082
Query 1147      ACTATGGCCAAAGGCCCGGGTACTCTCAGAGGGCTCGAGTCCCCATAATCAGCAATGATG 1206
Sbjct 1083      TCTATGGCCAAAGGCCCTATGGTGTCCAGAGGGCCCGGTTCCTCATTAAGCAACGAGAG 1142
Query 1207      TCTGCAATGGCGCTGACTCTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGTGCT 1266
Sbjct 1143      TTGTCAACAGGCCCGGACTTCTACGGGAATCAGATCAAGCCCAAGATGTTCTGTGCTGTGCT 1202
Query 1267      ACCCCGAGGGTGGCATTGATGCTCTGCCAGGGCGACAGCGTGGTCCCTTTGTGTGTGAGG 1326
Sbjct 1203      ATCTTCAGGGTGGCATTGATGCTGTCCAGGGCGACAGTGGAGGCCCTTTGTGTGTGAGG 1262
Query 1327      ACAGCATCTCTCGGACGCCACGTGTGGCGGCTGTGTGGCAATTGTGAGTTGGGGTACAGGCT 1386
Sbjct 1263      ACAGCATCTCTGGGACATCAAGGTGGCGGCTATGTGGCAATTGTGAGTTGGGGTACAGGCT 1322
Query 1387      GTGCCCTGGCCGAGGAGCCAGCGCTCTACACCAAAAGTCAGTGACTTCCGGGAGTGGAGTCT 1446
Sbjct 1323      GTGCTTGGCCCGGAGGCGCAGGGGTGTACACCAAAAGTCAGTGACTTCCGGGAGTGGAGTCT 1382
Query 1447      TCCAGGCCATAAAGACTCATTCTCGAAGCCAGCGGATGGTGAAGCCAGCTCTGA - CCGG - 1503
Sbjct 1383      TCAAGGCCATAAAGACTCATTCTCGAAGCCAGCTGGCTGTGTGACTCGAGCCCTGATCCGCC 1442
Query 1504      TGG-CT---T-CTC-G--CTGGGC-AGCCTCCAGGGGCCGAG -G-T--GAT--C-C-C-G 1545
Sbjct 1443      TCATCTCGCTGCTCGTGGCTGCTACAGCATCCAGAGTCAGAGTTGGTCTGTGTGCTCCAG 1502
Query 1546      -----GTGGTGGAGTCCACGCTGGGCCG-AGGATGGAGCGTTTCTCTCTGTGGCCCGG 1598
Sbjct 1503      CCCCACGTGGTAGGCTCCACACTGGGCCCTCAC-ATGGAAATGGTTCTCTGTCTCAGATCCAG 1561
Query 1599      TCCACAGGTCCTAAGGACACCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCACT 1658
Sbjct 1562      TCCACGGGTCCTAAGGATGC--TGGATCCAAAGGACTTCTCTTCCACAGTGGCGGCCACT 1619
Query 1659      CAGCCCC-GAGACCACCCAACTCACCCCTCTGACCCCCATGTAATATTGTGTTCTG-CTG 1716
Sbjct 1620      CAATCTCAGGG-CCATTGG-CTCACCCCTCCC-ACCCC-ATGTAATATTACTCTGTGCC- 1674
Query 1717      TCTGGGACTC-CTGTCTAGGT-GCCCTGATGATGG-GATGCTCTTTAAATAATAAAGAT 1773
Sbjct 1675      TCTGGGGGCGCT--CTAGGGAGCCCTC--TG-TGCAGATGCTCTTTAAATAATAAAGAT 1729
Query 1774      GGTTTTGTATT 1783
Sbjct 1730      GGTTTTGTATT 1739

```

>dbj|AK002694.1|  Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:061003A17 product:hepsin, full insert sequence  
Length=1814

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1181 bits (639), Expect = 0.0  
Identities = 1275/1573 (81%), Gaps = 80/1573 (5%)  
Strand=Plus/Plus

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Query 259      AGGGTGGCCGAGACTG-TGCCATGCTGCTCCAGACCCAGTGGCAGCTCTCATCTGCGGG 317
Sbjct 274      AGGGTGGCCGAGACTG-CAG-CATGCTGTCCAGACCCAGTGGCAGCTCTCATATTGGGT 332
Query 318      ACCCTGCTACTT-CTGACAGCCATCGGGCGGCATCTCGGCCATTGTGGCTTCTCTCT 376
Sbjct 333      ACCCTGCT-CTTCTGACAGGCAATTGGGGCGGCTCTCGGCCATTGTGACCATCTTACT 391
Query 377      -CAGGAGTGACCAAGAGACCGCTGTATCCCATGTGAGGTCTAGCT-CTGCGAGCGCTCGGCTC 434
Sbjct 392      GCA-GAGTGACCAAGAGGCACTGTATCCAGTGTGAGGTCTAG-TCAGGGGACATCGGGCTT 449
Query 435      ATGCTCTTTGACCAAGAGCGAGGG-AGTGGCGGCTGCTGTGCTCTCTGCGCTCCAAAGC 493
Sbjct 450      GCGGTGTTGACAGAGCGG-AAGGAACTGTGAAGGCTACTGTGCTCTCTACGCTCTCAAGT 508
Query 494      CAGGGTAGCCGAGACTCAGCTGGAGGAGATGGCTTCTCTCAGGGCACTGACCCATCCGGA 553
Sbjct 509      CAGGGTGGCAAGGCTCGGCTGTGAGGATGGCTTCTCTCAGGGCTCTGGCGCTCTAGGA 568
Query 554      GCTGGAAGCTGAGAAAGCGCGGGCGCAATGGCAAGTGGCGCTCTCTCTGTGTGAGAGAGGG 613
Sbjct 569      GCTGGATGTGCGCACTGCGGGCGCAACGCGACATCGGGCTCTCTTTGCGTGAAGCA-GG 627
Query 614      GAGG-CTGCCCCACACCCAGAGGCTGTCTGGAGGTCACTCTCGTGTGTGATGTGCCACAG 672
Sbjct 628      GCGGACTGCCCTGGCTCAGAGGTTGCTGGATGTCTCTCTGTATGTGACTGTCTTAGAG 687
Query 673      GCGCTTTCTTGGCCGCGCACTGCCAAAGCTGTGGCCGAGGAAGCTGCCGCTGAGACGCA 732
Sbjct 688      GCGGATTCCTGACTGCGCACTGCCAAGACTGTGGCCGCA-GAAGTGCCTGTGAGACGCA 746

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Query 733 TCGTGGGAGGCCGGGACACCAAGCT-TGGGCCGGTGGCCGTGGCAAGTCAGCCCTCGCTAT 791
Sbjct 747 TTGTGGGGGGCCAGGACAGCAG-TCTGGGAAGGTGGCCGTGGCAGGTACGCCCTGCTTAT 805
Query 792 GATGGAGCA-CACCTCTGTGGGGATCCCTGCTCTC-CGGGAGCTGGGTGTGTACAGCCG 849
Sbjct 806 GATGG-GTACCACTCTGTGGGGGT-CTGCTGTCTC-GGAGCTGGGTGTGTACAGCTG 862
Query 860 CCCACTGCTTCCCGAGG-GGA-ACCGGGTCTGTCCCGATGGCCAGTGTGTGGCCGTGC 907
Sbjct 863 CACTTGTCTTCCAGGCGGGGGA-C-GTCCCTGTCTGGGTGGCAGTATTTGCTGTGCT 920
Query 908 CGTGGCCCGAG-CCTCTCCCCAAGGTCTGAGCTGGGGGTGCAGGCTGTGTGTACACAG 966
Sbjct 921 TGTAGCCC-GAACCTCAACCCATGCTGTGCAACT-GGGGTTCAGGCTGTGTATTTATCATG 978
Query 967 GGGGCTATCTTCC-CTTTCGGGACCCCAAC-AGCGAGGAGAACAGCAAGATATTGCCCT 1024
Sbjct 979 GGGGCTA-CCTCTCTTTTGAGA-CCTTACTATCGAGGAACAGCATGATGATGCTT 1036
Query 1025 GGTCCACCTCTTCCAGTC-CCTGCCCCCTCACAAGATACATCCAGCTGTGTGTGCTCCAG 1083
Sbjct 1037 GGTCAACCTCTCTAG-CTCCCTGCTCTCACAAGATACATCCAGCAGTGTGTGTCTCCGT 1095
Query 1084 CTGCGGGGCAAGGCCCTGTGGATGGCAAGATCTGTACCGTGAACGGCTGGGGCAACGC 1143
Sbjct 1096 CTGCGGGGCAAGGCCCTGTGGATGGCAAGGTCTGTACTGTGACCGCTGGGGTAACACAC 1155
Query 1144 AGTACTATGGCCAAAGGCCGGGTACTCTCAGGAGGCTCGAGTCCCATATTCAGCAATG 1203
Sbjct 1156 AGTTCTATGGCCAAAGGCTATGGTGTCTCAAGAGGCCCGGGTTCCTCATATGAGCAAGC 1215
Query 1204 ATGTCTGAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTCTGTGCTG 1263
Sbjct 1216 AAGTTTGAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGATGTCTGTGCTG 1275
Query 1264 GCTACCCCGAGGGTGGCATTTGATGCTGCGAGGGCGACAGGGTGGTCCCTTTGTGTGTG 1323
Sbjct 1276 GCTATCTGAAGGTGGCATTTGATGCTGCGAGGGCGACAGGGTGGAGGCCCTTTGTGTGTG 1335
Query 1324 AAGACAGCATCTCTTGGAGCCGACGCTGGCGGCTGTGTGGCATTTGTGATGTGGGCACTG 1383
Sbjct 1336 AAGACAGCATCTCTTGGAGCCGACGCTGGCGGCTGTGTGGCATTTGTGATGTGGGCACTG 1443
Query 1384 GCTGTGCCCTGGCCCGAAGGACGGGCTCTACACCAAGTCAAGTCACTGACTTCCGGAGTGG 1455
Sbjct 1396 GCTGTGCTTTGGCCCGAAGGACGGGAGTGTACACCAAGTCAAGTCACTGACTTCCGGAGTGG 1463
Query 1444 TCTTCCAGCCCATAAAGACTCTACTCCGAAGCCGCGCATGTGTGACCCAGCTCTGA-CCG 1502
Sbjct 1456 TCTTCAAGCCCATAAAGACTCTACTCCGAAGCCGCGCATGTGTGACTGACCCAGCTCTGATCC 1515
Query 1503 G-TGG-CT---T-CTC-G-CTGCGC-AGCCCTCCAGGCCCGAG-G-T-GAT--C-C 1543
Sbjct 1516 GCCTCATCTGCTGCTCCGCTGCTGCACTAGCATCCAGAGTCAGAGTGTGTCTGTGGCTG 1575
Query 1544 C-G-----GTGGTGGGATCCACGCTGGGCG-AGGATGGGAAGTTTCTCTCTTGGGCC 1595
Sbjct 1576 CAGCCCCACGTGGTAGGCTCCACACTGGGCTCAC-ATGGAATGTTTCTCTCTGATGATG 1634
Query 1596 CGGTCCACAGGTGCCAAGGACACCTCCCTCCAGGGTCTCTCTTCCACAGTGGCGGGCCCC 1655
Sbjct 1635 CAGTCCACAGGTGCCAAGGATGC--TGGATCCAGGGACTTCTCTTCCACAGTGGCGGGCCCC 1692
Query 1656 ACTCAGCCCC-GAGACCAACCCACCTCACCTCCTGACCCCATGTAAATATTGTCTGTG- 1713
Sbjct 1693 ACTCAATCCCAAGG-CAATTGG-CCTCACCTCCCC-ACCCC-ATGTAAATATTACTCTGT 1748
Query 1714 CTGTCTGGGACTC-CTGTCTAGGT-GCCCTGATGATGG-GATGCTCTTTAAATATATAA 1770
Sbjct 1749 CC-TCTGGGGGGCGCT--CTAGGGAGGCCCT--TG-TGCAGTGTCTTTAAATATATAA 1802
Query 1771 GATGGTTTGTATT 1783
Sbjct 1803 GGTGGTTT-ATT 1814

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>ref|XM\_512584.2| **C** PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 3 (HFN), mRNA  
Length=1572

GENE ID: 455944 HFN | hepsin (transmembrane protease, serine 1)  
[Pan troglodytes]

Sort alignments for this subject sequence by:  
E value Score Percent identity  
Query start position Subject start position

Score = 1011 bits (547), Expect = 0.0  
Identities = 545/550 (99%), Gaps = 0/550 (0%)  
Strand=Plus/Plus

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Query 658 GTGATGCCCCAGAGGCCGTTTCTTGGCTGCCATCTGCCAAGACTGTGGCCGCAAGAGC 717
Sbjct 490 GTGATGCCCCAGAGGCCGTTTCTTGGCGCCCATCTGCCAAGACTGTGGCCGCAAGAGC 549

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Query 718  TGCCTCGGACCGCATCTGTGGAGGCGCGGACACAGCTTGGGCGGTGGCCGTGGCAAG 777
Sbjct 550  TGCCTCGGACCGCATCTGTGGAGGCGCGGACACAGCTTGGGCGGTGGCCGTGGCAAG 609

Query 778  TCAGCCCTTCGCTATGATGAGGACACCTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGGG 837
Sbjct 610  TCAGCCCTTCGCTATGATGAGGACACCTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGGG 669

Query 838  TGCTGACAGCCGCGCCACTGCTCTCCCGGAGCGGACCGGGTCTGTCCCGATGGCGAGTGT 897
Sbjct 670  TGCTGACAGCCGCGCCACTGCTCTCCCGGAGCGGACCGGGTCTGTCCCGATGGCGAGTGT 729

Query 898  TTGCGGGTGGCCGTGGCCCGAGGCTCTTCCCAAGGCTTGCAGCTGGGGGTGGCAGGCTGGG 957
Sbjct 730  TTGCGGGTGGCCGTGGCCCGAGGCTCTTCCCAAGGCTTGCAGCTGGGGGTGGCAGGCTGGG 789

Query 958  TCTACCAAGGGGGCTATCTTCCCTTTTGGGACCCCAACAGCGAGGAGAACAGCAGCAGATA 1017
Sbjct 790  TCTACCAAGGGGGCTATCTTCCCTTTTGGGACCCCAACAGCAGGAGAGAACAGCAGCAGATA 849

Query 1018  TTGCCCCTGGTCCACCTCTCCAGTCCCTTCCGCCCCACAGAAATACATCCAGCTGTGTGCC 1077
Sbjct 850  TTGCCCCTGGTCCACCTCTCCAGTCCCTTCCGCCCCACAGAAATACATCCAGCTGTGTGCC 909

Query 1078  TCCCGAGTGGCGGCGCAGGCGCTGGTGGATGGCGAGATCTGTACCGTGAAGCGGTGGGGCA 1137
Sbjct 910  TCCCGAGTGGCGGCGCAGGCGCTGGTGGATGGCGAGATCTGTACCGTGAAGCGGTGGGGCA 969

Query 1138  AACAGCAGTACTATGGCCCAACAGCCCGGGTACTCCAGAGGGCTGGAGTCCCATATATCA 1197
Sbjct 970  AACAGCAGTACTATGGCCCAACAGCCCGGGTACTCCAGAGGGCTGGAGTCCCATATATCA 1029

Query 1198  GCAATGATGT 1207
Sbjct 1030  GCAATGATGT 1039

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Score = 968 bits (524), Expect = 0.0  
 Identities = 528/530 (99%), Gaps = 0/530 (0%)  
 Strand=Plus/Plus

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Query 1254  TTCTGTGCTGGCTACCCCGAGGGTGGCATTTGATGCGCTGCCAGGGCGACAGCGGTGTGCC 1313
Sbjct 1041  TTCTGTGCTGGCTACCCCGAGGGTGGCATTTGATGCGCTGCCAGGGCGACAGCGGTGTGCC 1100

Query 1314  TTGTGTGTGAGGACAGCATCTCTCGGACGCCAGCTTGGCGGCTGTGTGGCATTTGTAGT 1373
Sbjct 1101  TTGTGTGTGAGGACAGCATCTCTCGGACGCCAGCTTGGCGGCTGTGTGGCATTTGTAGT 1160

Query 1374  TGGGGCACTGGCTGTGCGCTGGCCAGAGGCCAGGCGTTACACCAAAGTCAAGTATTC 1433
Sbjct 1161  TGGGGCACTGGCTGTGCGCTGGCCAGAGGCCAGGCGTTACACCAAAGTCAAGTATTC 1220

Query 1434  CGGGAGTGGATCTTCCAGGCCATTAAGACTCACTCCGAGGCGAGCGCATGGTGAACAG 1493
Sbjct 1221  CGGGAGTGGATCTTCCAGGCCATTAAGACTCACTCCGAGGCGAGCGCATGGTGAACAG 1280

Query 1494  CTCTGACCGGTTGGCTTCTGCGCTGCGCAGCTCCAGGGCCCGAGGTGATCCCGGTGTGGG 1553
Sbjct 1281  CTCTGACCGGTTGGCTTCTGCGCTGCGCAGCTCCAGGGCCCGAGGTGATCCCGGTGTGGG 1340

Query 1553  ATCCACGCTGGGCGAGGATGGGACGTTTTTCTTCTTGGGCGCGGTCCACAGGCTCAAGG 1613
Sbjct 1341  ATCCACGCTGGGCGAGGATGGGACGTTTTTCTTCTTGGGCGCGGTCCACAGGCTCAAGG 1400

Query 1614  AACACCTCCCTCCAGGGTCCCTCTCTTCCACAGTGGCGGGGCCCATCAGCCCCAGAGCCAC 1673
Sbjct 1401  AACACCTCCCTCCAGGGTCCCTCTCTTCCACAGTGGCGGGGCCCATCAGCCCCAGAGCCAC 1460

Query 1674  CCACACTCACCCCTCTGACCCCCCATGTAAATATTGTTCTGTCTGAGGATCTGTCTA 1733
Sbjct 1461  CCACACTCACCCCTCTGACCCCCCATGTAAATATTGTTCTGTCTGAGGATCTGTCTA 1520

Query 1734  GGTGCCCCGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTGGATT 1783
Sbjct 1521  GGTGCCCCGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTGGATT 1570

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Score = 638 bits (345), Expect = 3e-179  
 Identities = 345/345 (100%), Gaps = 0/345 (0%)  
 Strand=Plus/Plus

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Query 191  GGTCCCAACCTGGGCCAGGAGGTTCAGCCAGGGAATCATTAACAAGAGGCACTGATCATGCG 250
Sbjct 146  GGTCCCAACCTGGGCCAGGAGGTTCAGCCAGGGAATCATTAACAAGAGGCACTGATCATGCG 205

Query 251  GCAGAGGAGAGGGTGGCGGACGTGTGCCATGCTGCTCCAGACCCAGGTGGCAGCTCTCAC 310
Sbjct 206  GCAGAGGAGAGGGTGGCGGACGTGTGCCATGCTGCTCCAGACCCAGGTGGCAGCTCTCAC 265

Query 311  TGGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCTTGGGCCATTTGTGGTGT 370
Sbjct 266  TGGCGGGGACCTTGCTACTTCTGACAGCCATCGGGGCGGCATCTTGGGCCATTTGTGGTGT 325

Query 371  TCTCCTCAGAGTGAACAGAGGACGCGCTGTACCCAGTGCAGTCACTCTCGGACGCTCTG 430
Sbjct 326  TCTCCTCAGAGTGAACAGAGGACGCGCTGTACCCAGTGCAGTCACTCTCGGACGCTCTG 385


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Query 431 GCTCATGGTCTTTGACAAAGACGGAAGGACGTGGCGGCTGCTGTGCTCTCGCGCTCCAA 490
Sbjct 386 GCTCATGGTCTTTGACAAAGACGGAAGGACGTGGCGGCTGCTGTGCTCTCGCGCTCCAA 445

Query 491 CGCCAGGGTAGCCGGAATCAGCTGCGAGGAGATGGGCTTCCTCAG 535
Sbjct 446 CGCCAGGGTAGCCGGAATCAGCTGCGAGGAGATGGGCTTCCTCAG 490

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>gb|BC072688.1| Rattus norvegicus hepsin, mRNA (cDNA clone MGC:91742 IMAGE:7098661), complete cds  
Length=1580

GENE ID: 29135 Hpn | hepsin [Rattus norvegicus] [10 or fewer PubMed links]

Sort alignments for this subject sequence by:

E value Score Percent identity

Query start position Subject start position

Score = 935 bits (506), Expect = 0.0  
Identities = 828/983 (84%), Gaps = 23/983 (2%)  
Strand=Plus/Plus

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Query 184 ACCCCAGGGTCCCACTCTGACCGGAGGAGTTCAGCCAGGGAATCATTAACAAGAGGCAAGTG 243
Sbjct 27 ACCCCAGGGTCTCGCCCCGAGCCCAACAGGTCAACTTGGGAATCATTAACAAGAGTCCCTG 86

Query 244 ACATGAGCGAGAGAGGAGGAGTGGCCGAGCTGTGCCATCTGCTCCAGACCCAGGTGGCAG 303
Sbjct 87 ACAT-G-GC-GAAGGAGGAGTGGCCGAGCTGCAACATGCTGTTCAGAGCCCAAGGTGGCAG 143

Query 304 CTCTCACTGCGGGGACCCCTGCTACTTC-TGACAGCCATCGGGGCGGCATCTGGGCCATT 262
Sbjct 144 CTCTCACTGTGAGGACCCCTGCTG-TTCTTGACAGGCAATTGGGGCTGCGCTCTGGGCCATT 303

Query 363 GTGGCTGTCTCTCT-CAGAGGTGACACGAGGCGCGCTGTACCAAGTGCAGGTGAG-CTTG 420
Sbjct 203 GTGACCATCTTACTAC-GGAGTGAACGAGAGCCACTGTACCAAGTGCAGGTGAGTCCCG 261

Query 421 CGGACGCTCGGCTCATGCTCTTTGACAAAGCGGAGAGGA-CGTGGCGGCTGCTGTGCTCC 479
Sbjct 262 -GGACTCTGAGCTTTTGGTGTGAGCAAGACAG-GGAGAACGTGAGAGGCTGTGCTGCTCC 319

Query 480 TGGCGCTCCAAAGCCAGGAGTGGCCGAGCTCAGCTGCGAGGAGATGGGCTTCCTCAGGACA 539
Sbjct 320 TCAAGCTCCAAAGCCAGGAGTGGCCGAGCTCAGCTGAGAGATGGGCTTCCTCAGGACT 379

Query 540 CTGACCCACTCCGAGCTGAGCTGCGAAGCGCGGGCCGCAATGGCAGCTCGGGCTTCTTC 599
Sbjct 380 CTGAGCGCACTCAGAGCTGAGTGTGCGAAGCGCGGGCCGCAAGCGCACTCGGGCTTCTTC 439

Query 600 TGTGTGGAAGAGGGGAGG-CTGCCCCACACCCAGAGGCTGTGCGAGGTCACTCTCCGTGTG 658
Sbjct 440 TGCSTGGAAGAGGAC-GGTCTGCTCTGCTGCTGAGCGGTGTGCGAGGTCACTCTCTGTATG 498

Query 659 TGATTGCCCCAGAGGCCGTTTCTTGGCGCCATCTGCCAAGACTGTGGCCGAGGAAGCT 718
Sbjct 499 CGACTGTCTTGAAGGCCGATTCCTGACTGCCACTGCAAGACTGTGGCCGAGGAAGCT 558

Query 719 GCCCGTGGACCGCATCTGTGGAGAGCGCGGACACCAAGCTTGGGCCGGTGGCCCGTGGCAAGT 778
Sbjct 559 GCGCGTGGATGCACTTGTGGGGGGCCAGGACAGCAAGCTTGGGAAGATGGCCATGGCAGGT 618

Query 779 CAGCCTTCGCTATGATGG-AGCAGCCTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGG 837
Sbjct 619 CAGCCTTGGGTTATGATGGGACC-CACCTCTGTGGGGGATCCCTGCTCTCCGGGAGCTGG 677

Query 838 TACTGACAGCGCCCACTGCTTCCCGGAGCGGGAACCGGGCTCTGTCCCGATGGAGGTGT 897
Sbjct 678 TACTGACCGCTGACACTGCTTTCAGAGGAGAACCGGGCTCTGTCTCGGTGGAGGTAT 737

Query 898 TTGCGCGTGGCGTGGCGGAG-CCTCTTCCCAAGGTG-TGCACTGGGGGGTGGCAGCTGTG 955
Sbjct 738 TTGCTGGTGGCTGAGCCC-GGAAGCTCACTATGTC-CTGTCAGCTGGGGGGTGTGAGGTGT 795

Query 956 GGTCTACCAAGCGGGGCTATCTTCCCTTTTGGGAGCCCCAC-AGCGAGGAGAGCAGCAAG 1014
Sbjct 796 GATCTATCATGGGGGCTACTCTTCCCTTTTGGAGCCCTA-CTATGACAGAAACAGCAATG 854

Query 1015 ATATTGCGCTGATCCACTCTCTCAG-TCCCTGCGCCCTCAGAGAAATACATCAGAGCTGTG 1073
Sbjct 855 ACATTGCGCTGATCCACTCTCTAGCTCCC-TGCCCTCAAGAGAAATACATCAGAGCGGTG 913

Query 1074 TGCTCCCGAGCTGCGCGGACGAGCGCTGGTGGATGGCAAGATCTGTGACCTGTGACGGCTGG 1133
Sbjct 914 TGTCTCCCTGCTGCGGACAGGCGCTGGTGGACGGCAAGTCTGTACAGTGAACCGCTGG 973

Query 1134 GGCAACACGCGAGTACTATGAGCCA 1156
Sbjct 974 GGTAAACACAGTCTCTATGAGCCA 996

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Score = 265 bits (143), Expect = 6e-67  
Identities = 405/525 (77%), Gaps = 44/525 (8%)  
Strand=Plus/Plus

Query 1291 GCCAGGGGAGCAGCGGTGGTCCCTTGTGTGTGAGGACGACATCTCTCGG-ACGCCAAGT 1349

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Sbjct 993      |G|CCAGGGTGACAGCGGAGGCCCCCTTGTATGTGAGGACAGATCTCT- GGAAATCATAGAA 1051
Query 1350      |G|TGGCGCTGTGTGACATTGTGAAGTTGGGGCACTGGCTGTGGCCCTGGCCAGAGCCAGGC 1409
Sbjct 1052      |G|TGGCGCTGTGTGACATTGTGAAGTTGGGGCACTGGCTGTGGCCCTGGCCAGAGCCAGGC 1111
Query 1410      |G|GTCTACACCAAAAGTCATGTGACTTCCCGGAGTGGATCTTCCAGGCCATAAAGACATCACTCC 1469
Sbjct 1112      |G|GTCTACACCAAAAGTCATGTGACTTCCCGGAGTGGATCTTCCAGGCCATAAAGACATCACTCC 1171
Query 1470      |G|GAAGCCAGCGGCAATGTGTAACTCAGCCCTCTGACCGG-G-TG---GCTT-CTC-G--TGCGC 1519
Sbjct 1172      |G|GAAGCTACCGGCAATGTGTAACTCAGCCCTGACCCCGCTCATGCGCTGCTCGCGCTGCTC 1231
Query 1520      |G|-AGCCTCCAGGGCCCGGAG--G-T--GAT--C-CCGGT-G--GTGGGA--TCCACGCTC 1563
Sbjct 1232      |G|CAGCATCCAGAGTCAGAGTTGTGCTGTGTGGCTCAGACCGCATCGTGGCAGGCTCCACACTG 1291
Query 1564      |G|GGCGG-AGGATGGGACGTTTTTCTTCTGGGCCCGGTCACAGGTCCAAAGAACACCCCTCC 1622
Sbjct 1292      |G|GGCTCAC-ATGGAAACGGTTTTTCTGCTCGGATCCAGTCCATAGATCCAAAGATGC--TGG 1348
Query 1623      |G|CTCCAGGGTCCCTCTCTTCCACAGTGGCGGGCCCATCTCAGCCCC-GAGAACCCACCACTTC 1681
Sbjct 1349      |G|CTCCAGGGCTCTCTCTTCCACAGTGGCGGGCCCATCTCAGCCCC-GAGAACCCACCACTTC 1406
Query 1689      |G|ACCCCTCTGACCCCCATGTAAATTTGTGTCG-CTGCTGGGA-CTCCTGTCTAGGTGTC 1739
Sbjct 1407      |G|ACCCCTCC-ACCCC-ATGTAAATTTTACTCTGTCC-CTGCGGGGCTGCTTTGAGGCGCC 1463
Query 1740      |G|CCTGATGATG-GGATGCTCTTTAAATAATAAAGATGGTTTGTGATT 1783
Sbjct 1464      |G|CCT--TG-TGCAGATGCTCTTTAAATAATAAAGATGGTTTGTGATT 1505

```

gb|AY234104.1| **G** Mus musculus truncated hepsin splice variant mRNA, complete cds;  
 alternatively spliced  
 Length=1887

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Sort alignments for this subject sequence by:  
 E value    Score    Percent identity  
 Query start position    Subject start position

Score = 880 bits (476), Expect = 0.0  
 Identities = 944/1164 (81%), Gaps = 56/1164 (4%)  
 Strand=Plus/Plus

```

Query 658      |G|GTGATTGCCCCAGAGGCGGTTTCTTGGCGGCCATCTGCCAAGACTGTGGCCGCGAGGAAGC 717
Sbjct 720      |G|GTGACTGTCTCAGAGGCGGATTTCTGACTGCCACCTGCCAAGACTGTGGCCGCGAGGAAGC 779
Query 718      |G|TGCCCGTGGACCGCATCTGTGGAGGCGGGACACCG-CTTGGGCGGTTGGCCGTGGCAA 776
Sbjct 780      |G|TGCCCGTGGACCGCATCTGTGGAGGCGGGACACCGTCT-GGGAGGTTGGCCGTGGCAG 838
Query 777      |G|GTCAAGCTTCTGCTATGATGG-AGCACCTCTGTGGAGGATCCCTGCTCTCGGGAGCTG 835
Sbjct 839      |G|GTCAAGCTTCTGCTATGATGGAGCC-CACCTCTGTGGGGGTCCCTGCTGCTGGGGAGCTG 897
Query 836      |G|GTGCTGACAGCCGCCCACTGTCTCCCGGAGCGGAACCGGTCCTGTCCCGATGGCAGAT 895
Sbjct 898      |G|GTGCTGACTGCTGCATGTGCTTCCAGAGCGGAACCGGTCCTGTCTCGGTGGCAGAT 957
Query 896      |G|TTTTCGCGGTGCGGTGGCCGAGG-CTCTCTCCCAAGGCTCTGACGTGGAGGTTCAGGCTG 954
Sbjct 958      |G|TTTTCGCGGTGCGGTGGAGCCC-GGACCTCACCCCATGCTGTGCACTGGAGGTTCAGGCTG 1016
Query 955      |G|TGTCTACCAACCGGGGCTATCTTCCCTTTTGGGACCCCAAC-AGCAGAGGAGAACAGCAAC 1013
Sbjct 1017      |G|TGTCTATCATGGGGGCTATCTTCCCTTTTGGAGCCCTTA-CTATTGACGAAACAGCAAT 1075
Query 1014      |G|GATATTGCCCTGTGCTCACTCTCCAG-TGCCCTGCCCTCAAGAGATCATCTCAGGCTGT 1072
Sbjct 1076      |G|GATATTGCCCTGTGCTCACTCTTGTGCTGCC-TGCCCTTCACAGAGATCATCTCAGGCTGT 1134
Query 1073      |G|TGCTCTCCAGCTGCGCGGCGGCGCTGTGGTGGAGAGATCTGTATCCGTTGAGGGCTG 1132
Sbjct 1135      |G|TGCTCTCCAGCTGCGCGGCGGCGCTGTGGTGGAGAGATCTGTATCCGTTGAGGGCTG 1194
Query 1133      |G|GGGCAACAGCAGTACTATGGCCAAACAGGCGGGGTATCTCCAGGAGGCTGAGTCCCCAT 1192
Sbjct 1195      |G|GGTAAACACAGTACTATGGCCAAACAGGCTATGTGTCTCCAGAGGCTGAGTCCCAT 1254
Query 1193      |G|AATCAGCAATGATGTCTGCAATGGCGTGACTCTATGGAAACAGATCAAGCCAGAT 1252
Sbjct 1255      |G|CATAGCAACAGATTTGCAACAGCCCGACTCTTACCGGATCATAGATCAAGCCAGAT 1314
Query 1253      |G|TTCTGTGCTGGCTACCCCGAGGGTGGCATTTGATGCTGCCAGGGCGACAGCGTGTGTC 1312
Sbjct 1315      |G|TTCTGTGCTGGCTATCTTGAAGGTGGCATTTGATGCTGCCAGGGCGACAGTGGAGGCC 1372
Query 1313      |G|TTTGTGTGTGAGGACAGCATCTCTGGACGCCACGTGTGGCGGCTGTGTGGCATTTGTGAG 1374
Sbjct 1375      |G|TTTGTGTGTGAGGACAGCATCTCTGGACATCAAGGTGGCGGCTATGTGGCATTTGTAG 1434

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Query 1373 TTGGGGCACTGGCTGTGCGCTTGGCCAGAGCCAGGCGTCTACACCAAAGTCACTGACTT 1432
Sbjct 1435 TCGGGGTACCGGCTGTGCTTTGGCCCGGAGCCAGGAGTGTACACCAAAGTCACTGACTT 1494
Query 1433 CCGGAGGTGGATCTTCCAGGCGCATAAAGACTCACTCCGAGAGCCAGCGCATGTGTACCCA 1492
Sbjct 1495 CCGGAGGTGGATCTTCCAGGCGCATAAAGACTCACTCCGAGAGCCAGCGCATGTGTACCCA 1554
Query 1493 GCTCTGA-CGG--TGG-CT--T-CTC-G--CTGCGC-AGCCTCCAGGCGCCGAG--G- 1537
Sbjct 1555 GCTCTGAATCCCGCCTCATCTGCTGCTCCCGTGTGGTACTAGCATCCAGAGTCAAGATTGG 1614
Query 1538 T--GAT--C-CC-G-----GTGGTGGGATCCACGCTGGGCGG-AGGATGGGACGTTTTT 1584
Sbjct 1615 TCTGGTGGCTCCAGCCCCACGTGGTGAAGCTCCACCTGCGGCTCCAC-ATGGATGGTTTC 1673
Query 1584 CTCTTGGGCGCGTCCACAGGTCCAAAGACACCTCCCTCCAGGGTCTCTCTCTCCACA 1644
Sbjct 1674 CTCTCAGATCCAGTCCAGGGCTCAAGGATGC--TGGATCCAAAGATCTCTCTCCACA 1731
Query 1645 GTGGCGGGCCCACTCAGGCCCC--GAGACCCCAACTCACCCTTCGAGCCCCCATGTAAAA 1703
Sbjct 1732 GTGGCGGGCCCACTCAATCCCAAGG-CAATTGG-CCTCACCCTCC--ACCCC-ATGTAAA 1787
Query 1704 TATTGTTCTG-CTGCTTGGGACTC-CTGTCTAGGT-GCCCCGTGATGAGTGG-GATGCTCTT 1759
Sbjct 1788 TATTACTCTGTCC-CTTGGGGGCGCT--CTAGGAGCCCC--TG-TGCAGATGCTCTT 1841
Query 1760 TAAATAATAAAGATGGTTTGTATT 1783
Sbjct 1842 TAAATAATAAAGTGGTTTGTATT 1865


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Score = 403 bits (218), Expect = 1e-108  
 Identities = 394/477 (82%), Gaps = 19/477 (3%)  
 Strand=Plus/Plus

```

Query 184 ACCCCAGGGTCCCACTCTGGCCAGGAGGTGAGCGGGAATCATTAACAAGAGGCACTG 243
Sbjct 143 ACCCCAGGGTTCGCGCCCAAGCCCAAGGTCAACCTGGGATCATTAACAAGAGTCCCTG 202
Query 244 ACATGGCGCGAAAGGAGGGTGGCGGACTG-TGCCATGCTGCTCCAGACCCAGGTGGCA 302
Sbjct 203 ACAT-G-GC-GAAGAGGGTGGCGGACTGAGC-CATGCTGCTCCAGACCCAGGTGGCA 258
Query 303 GCTCTCACTGCGGGGACCCCTGCTACTTC-TGACAGCCATCGGGGCGGCTTCGGGCCAT 361
Sbjct 259 GCTCTCATTTGTGGGTACCCCTGCTG-TTCTTGACAGGCATTTGGGGCCGCTCTGGGCCAT 317
Query 362 TGTGGCTGTTCTCTCT-CAGGAGTGACAGGAGCGCGTACTACCAAGTGCAGGTCAAGTCT- 419
Sbjct 318 TGTGACCATCTTACTGAG-AGTGACCAAGGACCATGTACCAAGTGCAGGTCAAG-TCGA 375
Query 420 GCGGACGCTCGGCT--CATGGTCTTTGACAAGCGGAAGGG-ACGTGGCGGCTGTGTGC 476
Sbjct 376 GGGGACTCACGACTTGCA-G-TGTTGACAGAGCGGA-GGGTACGTGAGGCTTACTGTGC 432
Query 477 TCTTCGCGCTCCAAAGCCAGGGTAGCGGACTCAGCTGCGAGGAGATGGGCTCTCCAGG 536
Sbjct 433 TCTTCACGCTCCAAATGCCAAGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTTCTCAGG 492
Query 537 GCATGACCCCACTCCGAGCTGGAGCTGGAGACGGCGGGCGCCAAATGSCACGTGGGGCTTC 596
Sbjct 493 GCTCTGGCGCATCTGGAGCTGGAGTGGCGCATGCGGGCGCCAAAGCGCATCTGGGGCTTC 552
Query 597 TTTCTGTGTGAGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCACTTC 652
Sbjct 553 TTTTCGTGTGAGAGGGGCG-GAATCTCTCTTGGCTGAGAGGTGTCTGAGTGTCACTTC 608

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>ref|XM\_001254640.1|  PREDICTED: Bos taurus similar to hepsin (LOC787164), partial mRNA  
 Length=779

GENE ID: 787164 LOC787164 | similar to hepsin [Bos taurus]

Score = 815 bits (441), Expect = 0.0  
 Identities = 662/761 (86%), Gaps = 46/761 (6%)  
 Strand=Plus/Plus

```

Query 1052 CACAGATATCATCCAGCCTGTGTGCTCCAGCTCCCGGCCAGGCCCTGGTGGATGGCAA 1111
Sbjct 34 CACAGATATCATCCAGCCTGTGTGCTCCCGGCCAGGCCCTGGTGGATGGCAA 93
Query 1112 GATCTGTACCGTGAAGCGGCTGGGCAACACGAGTACTATGGCCACAGCGCCGGGTACT 1171
Sbjct 94 GATCTGTACCGTGAAGCGGCTGGGCAACACGAGTACTATGGCCACAGCGGCTGGGTACT 153
Query 1171 CCGAGAGGCTCGAGTCCCCAATAACAGCAATGATGTCTGCATATGGCTGACTTCTATGG 1231
Sbjct 154 CCGAGAGGCTCGAGTCCCCAATAACAGCAATGATGTCTGCATATGGCTGACTTCTACGG 213
Query 1232 AAACACAGATCAAGCCCAAGATGTTCTGTGTGCTGCTACCCCGAGGGTGGCAATTGATGCTG 1291
Sbjct 214 GAACACAGATCAAGCCCAAGATGTTCTGTGTGCTGCTACCCCGAGGGTGGCAATTGATGCTG 273

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Query 1292  CCAGGGCGACACGGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGAGGCCACGTTG 1351
Sbjct 274    CCAGGGCGACACGTGGTGGCCCCCTTCGTGTGTGAGGATAGCATCTCTCGAGGCCACGTTG 333

Query 1352  GCGGCTGTGTGGCATTGTGAAGTTGGGGCACTGGCTGTGCCCTGGCCCAGAAAGCCAGGGGT 1411
Sbjct 334    GCGGCTGTGTGGCATTGTGAAGTTGGGGCAACGGCTGTGCCCTGGCCCAGAAAGCCAGGGGT 393

Query 1412  CTACACCAAAGTCACTGATCTTCGGGAGTGGATCTTCAGGCCATAAAGACTCACTCCGA 1471
Sbjct 394    CTACACCAAAGTCACTGATCTTCGGGAGTGGATCTTCAGGCCATAAAGACTCACTCCGA 453

Query 1472  AGCCAGCGGATGTGACCCAGCTCTACCGCTGGGCTTCTC---GCTGCGCA-GCTTCCA 1527
Sbjct 454    AGCCAGCGGATGTGATCCAGCTCTTGAAGCTGTGGCTTCTCTCGCTGTGCAAGCTTCCA 513

Query 1528  GGGCCCGAGGTGATC-----CC-----G-----GTGGTGGGATCCAGCTGGGGCGAGG 1571
Sbjct 514    GGGCCCGAGGTGATCTAAAGGGGCCCCAGCCCCAGCTGATGGGGTTACCTCTGGCC-AGG 572

Query 1572  -ATGGAGAGCTTTTTTCTTTCTGGGGCCGGTCCACAGGTCCCAAGGACACCCCT-CCCTCCAGG 1629
Sbjct 573    GATGGAACTTTTTTCTTTCTTGGGGCCAGGCCACAGGTCCCAAGGATCTCTTCCCTCCAGG 632

Query 1630  GTCTCTCTTTCACAGTGGCGGGCCCACTCAGCCCCGAGACCAACCAACCTCAACCTCTCT 1689
Sbjct 633    GTCTCTC-C---ACAGTGGCGGGCCCACTCAGCCCTGGGACCAACCC---TC-TC-G-TC- 679

Query 1690  GAACCCCATGTAAATATTTGTTCTGTCTGTCTGGGA-CTCTGTG-----TCTAGAGGCTCT 1742
Sbjct 680    --CCCCCATGTAAATATTTGTTCTGTCTGTCTGGGATCCCCCCCCCATCTGTG-TGCTCT 736

Query 1743  GATGATGGGATGCTCTTTTAAATAAATAAGATGGTTTGGATT 1783
Sbjct 737    GAAGACAGGATGCTCTTTTAAATAAATAAGATGGTTTGGATT 777

```

>gb|BC119448.1| Mus musculus cDNA clone IMAGE:40044314  
Length=772

Score = 717 bits (388), Expect = 0.0  
Identities = 633/752 (84%), Gaps = 14/752 (1%)  
Strand=Plus/Minus

```

Query 448    AAGACGGAGAGGG-ACGTGGCGGCTGCTGTGCTCTCGCGCTCCAAAGCCAGGGTAGCGGA 506
Sbjct 761    AGA-GGATGGGAACTGGAGGCTACTGTGCTCTCAAGCTCCATGCCAGGGTGGCAGGG 703

Query 507    CTCAGCTGCGAGGAGTGGGCTTCTCAGAGGCACTGAACCACTCCGAGCTGAGAGTGGGA 566
Sbjct 702    CTCAGCTGTGAGGAGTGGGCTTCTCAGAGGCACTGTGACACTCGGAGCTGAGTGTGCC 643

Query 567    ACGCGGGCGCCAAATGGCAGCTGGGGCTTCTTCTGTGTGGAAGAAGGGAGG-CTGCCCCA 625
Sbjct 642    ACTCCGCGGCCCAACGGCAGCTATCGGCTTCTTTTGTGTGGAAGA-GGGCGAGTGGCTCT 584

Query 626    ACCCGAGAGGCTGCTGGAGGTCACTCCGTGTGTGATTCGCCAGAGGCCCTTCTTGTGGC 685
Sbjct 583    GGTCTAGAGGTTCCTGGATGTCACTCTGTATGTGACTGTCTTAGAGGGCCGATTCCTGAC 524

Query 686    CGCCCATCTGCACAGACTGTGGCCGACAGAACTGCCCGCTGGACCCGATCTGTGGAGGCCG 745
Sbjct 523    TGCCACCTGCCACAGACTGTGGCCGACAGAACTGCCCGCTGGACCCGATCTGTGGAGGCCA 464

Query 746    GGACACACAG-CTTGGGCGCGTGGCGCTGGCAAGTCAAGCTTCGCTATGATGG-AGCACG 803
Sbjct 643    GGAACAGAGTCT-GGGAAAGTGGCGCTGGCAGGTCAAGCTTCGCTATGATGGAGC-CAC 406

Query 804    CTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCCGCCACTGTCTCCCG 863
Sbjct 405    CTCTGTGGGGGATCCCTGCTGTCTGGGGACTGGGTGCTGACAGCTGCTGACATGTCTTCCA 346

Query 864    GAGCGGAACCGGGTCTCTCCGAGTGGCGAGTGTGTCGGGTGGCGGTGGCCAGG-CTCT 922
Sbjct 345    GAGCGGAACCGGGTCTCTCTCGTGGCGAGTATTTGCTGGTGTCTGTAGCCC-GGACCTC 287

Query 923    TCCCCAGGCTCTGACAGCTGGGGGTGCAAGGCTGTGGTCTACCAAGGGGGCTATCTTCCCT 982
Sbjct 286    ACCCCATGCTGTGCAACTGGGGGTTCAGGCTGTGATCTATCTATGAGGGGTACCTCTCCCT 227

Query 983    TGGGAGCCCCAAC-AGCGAGAGAGACAGACAGATATTGCCGTGTGCTCAACCTGCTCAG-T 1040
Sbjct 226    TCGAGACCTTA-CTATCGAGCAAAACAGCAATGACATTGCTCTGTGCTCACTCTCTAGCT 168

Query 1041  CCCCCTGCCCTCAGAGAAATACATCCAGCCTGTGTGCTCCGAGCTGGCGGACAGGCCCTG 1100
Sbjct 167    CCC-TGCCCTCTCAGAGAAATACATCCAGCAGTGTGTCTCCCTGCTGGGGAAGAGCCCTG 109

Query 1101  GTGGATGGCAAGATCTGTACCTGTACCGGCTGGGGCAACACGAGTACTATGGCCACAG 1160
Sbjct 108    GTGGATGGCAAGTCTGTACTGTGACCGGCTGGGGTAAACACAGATTTATGGCCACAG 49

Query 1161  GCCGGGGTACTCCAGAGGCTCGAGTCCCCCAT 1192
Sbjct 48    GCTATGGTGTCCAGAGGCGCCGGGTCCCAT 17

```

>gb|BC119449.1| Mus musculus cDNA clone IMAGE:40044315

Length=772

Score = 712 bits (385), Expect = 0.0  
 Identities = 632/752 (84%), Gaps = 14/752 (1%)  
 Strand-Plus/Minus

```

Query 448 AGACGGAGGGG-ACTGCGCGCTGCTGTGCTCTCTGCGCTCCAAAGCCAGGGTAGCGGA 506
Sbjct 761 AGA-GGATGGGAACCTGGAGGCTACTGTGCTCTCAAGCTCCAAATGCCAGGGTAGCAAGG 703

Query 507 CTTCAGCTGCGAGAGAGATGGGCTTCTTCAGGGCACTGACCCCACTCCAGCTGAGCTGCGA 566
Sbjct 702 CTTCGGCTGTGAGAGAGATGGGCTTCTTCAGGGCTCTGGCACTCTCGAGCTGAGATGTGCGC 643

Query 567 ACGGCGGGGCGCCAAATGGCACTGCGGGCTTCTTCTGTGTGGAAGAGGGAGG-CTGCCCCA 625
Sbjct 642 ACTGCGGGGCGCCAAAGGCACTGGGGCTTCTTTTACGTGGAAGA-GAGCGAGCTGCTCTCT 584

Query 626 CACCCAGAGGGCTGTGAGAGTCACTCTCGTGTGTGATTGCCCCAGAGGCGCTTCTTGGC 685
Sbjct 583 GGCTCAGAGGGTGTGAGATGTCACTCTGTATGTGACTGTCTCTCAGAGGCCGATTCCTGAC 524

Query 686 CGCCACTCTGCAAGACTGTGGCGGCAAGAGCTGCCCGTGGACCGCATGTGGAGGGCCG 745
Sbjct 523 TGCCACCTGCCAAGACTGTGGCGGCAAGAGCTGCCCGTGGACCGCATGTGGAGGGCCCA 464

Query 746 GGACACCAG-CTTGGGCGGGTGGCGGTGGCAAGTCAGGCTTCGCTATGATGG-AGCACAC 803
Sbjct 463 GGACAGCAGTCT-GGGAAGGTGGCGGTGGCAAGTCAAGCTTCGCTATGATGGAGC-CAC 406

Query 804 CTCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCGCGCCACTGCTCCCG 863
Sbjct 405 CTCTGTGGGGGATCCCTGCTCTGCGGGACTGGGTGCTGACAGCTGCTGCAATGTCTTCCA 346

Query 864 GAGCGGAACCGGGTCTCTCCGATGGCGAGTGTTCGCGGTGCCGTGGGCCAGG-CTTC 922
Sbjct 345 GAGCGGAACCGGGTCTCTCGTGGGAGATTTGCTGGTGTCTGTAGCCC-GAGACTTC 287

Query 923 TCCCCACGGTCTGACAGCTGGGGGTGACGGCTGTGGTCTACCAAGCGGGCTATCTTCCCTT 982
Sbjct 286 ACCCCATGCTGTGCACTTGGGGGTTCAGGCTGTGATCTATCATGGGGGCTACTCTCCCTT 227

Query 983 TGGGAGCCCCAAC-AGCGAGGAGAGACGCAACGATATTGCCCTGGTCCAACTCTCAGG-T 1047
Sbjct 226 TGGAGACCCCTA-CTATGACGAGAAACAGCAATGACATTGCCCTGGTCCAACTCTCAGCT 168

Query 1041 CCCCCTGCCCTCAGAGAAATATCCAGGCTGTGTGCCCTCCAGCTGCGGGCAGGGCCCTG 1100
Sbjct 167 CCC-TGCCCTCTCAGAGAAATATCCAGGCACTGTGTCTCCCTGCTCGGGGACAGGCCCTG 109

Query 1101 GTGGATGGCAAGATCTGTGACCTGTGACCGGCTGGGGCAACACAGCATATCTATGGCCAAACG 1160
Sbjct 108 GTGGATGGCAAGTCTGTACTGTGACCGGCTGGGGTAACACAGCATCTCTATGGCCAAACG 49

Query 1161 GCCCGGGTACTCCAGGAGGCTCGAGTCCCAT 1192
Sbjct 48 GCTATGGTGTCTCAAGAGGCGCCGGGTCCCAT 17

```

>gb|AC192150.4| Pan troglodytes BAC clone CH251-522E19 from chromosome 19, complete  
 sequence  
 Length=213011

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165  
 Identities = 323/325 (99%), Gaps = 0/325 (0%)  
 Strand-Plus/Plus

```

Query 1459 AGACTCACTCCGAAGCCAGCGGATGGTGACCCAGCTCTGACCGGTGGCTTCTGCTGCG 1518
Sbjct 179133 AGACTCACTCCGAAGCCAGCGGATGGTGACCCAGCTCTGACCGGTGGCTTCTGCTGCG 179132

Query 1519 CAGGCTCCAGGGCCCCGAGGTGATCCCGGTGGTGGGATCCAGCTGGGCCGAGGATGGGAC 1578
Sbjct 179193 CAGGCTCCAGGGCCCCGAGGTGATCCCGGTGGTGGGATCCAGCTGGGCCGAGGATGGGAC 179252

Query 1579 GTTTTCTCTCTTGGGCCCCGGTCCACAGGTCCAGGACACCCCTCCCTCAGAGGTCTCTCT 1638
Sbjct 179253 GTTTTCTCTCTTGGGCCCCGGTCCACAGGTCCAGGACACCCCTCCCTCAGAGGTCTCTCT 179312

Query 1639 TCACACGTGGCGGGGCCACTCAGCCCCGAGACACCCAACTCACCCTCTGACCCCCCAT 1698
Sbjct 179313 TCACACGTGGCGGGGCCACTCAGCCCCGAGACACCCAACTCACCCTCTGACCCCCCAT 179372

Query 1699 GTAAATATTGTTCTGCTGTCTGGGACTCCGTCTAGGTGCCCTGATGATGGATGCTCT 1758
Sbjct 179373 GTAAATATTGTTCTGCTGTCTGGGACTCCGTCTAGGTGCCCTGATGATGGATGCTCT 179432

Query 1759 TTAAATAATAAGATGGTTTGAATT 1783
Sbjct 179433 TTAAATAATAAGATGGTTTGAATT 179457

```

Score = 348 bits (188), Expect = 6e-92

Identities = 198/202 (98%), Gaps = 3/202 (1%)  
Strand=Plus/Plus

```

Query 858      TTCCC-GG-A-GCGGAAACCGGTCCTCTCCGATGGCAGTGTGTCGGTGCCTGGCC 914
Sbjct 173569   TTCCCCTGGTAAGCGGAAACCGGTCCTCTCCGATGGCAGTGTGTCGGTGCCTGGCC 173628

Query 915      CAGGCGCTCTCCCAACGCGCTGCAAGCTGGGGGTGAGGCTGTGGTCTAACACGCGGGCTAT 974
Sbjct 173629   CAGGCGCTCTCCCAACGCGCTGCAAGCTGGGGGTGAGGCTGTGGTCTAACACGCGGGCTAT 173688

Query 975      CTTCCTCTTCGGGAGCCCAACAGCAGGAGGAGAACAGCAACGATATTGCGCTGTCTCACCTC 1034
Sbjct 173689   CTTCCTCTTCGGGAGCCCAACAGCAGGAGGAGAACAGCAACGATATTGCGCTGTCTCACCTC 173748

Query 1035     TCCAGTCCCGCTGCCCTCAGAG 1056
Sbjct 173749   TCCAGTCCCGCTGCCCTCAGAG 173770

```

Score = 315 bits (170), Expect = 6e-82  
Identities = 172/173 (99%), Gaps = 0/173 (0%)  
Strand=Plus/Plus

```

Query 1288     CTTGCGCAGGCGCAGCAGCGTGTGTCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 1347
Sbjct 178746   CTTCCACAGGCGCAGCAGCGTGTGTCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 178805

Query 1348     GTTGGCGAGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGGCCCTGGCCAGGACCTC 1407
Sbjct 178806   GTTGGCGAGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGGCCCTGGCCAGGAGCCAG 178865

Query 1408     GCGCTCTACACAAAGTCACTGACTTCCGGGAGTGGATCTTCCAGGCCATATAAG 1460
Sbjct 178866   GCGCTCTACACAAAGTCACTGACTTCCGGGAGTGGATCTTCCAGGCCATATAAG 178918

```

Score = 313 bits (169), Expect = 2e-81  
Identities = 172/173 (99%), Gaps = 1/173 (0%)  
Strand=Plus/Plus

```

Query 695      CCA-AGACTGTGTGGCGCAGGAGGCTGCCCGTGGACCGCATGTGGGAGGCCGGGACACCA 753
Sbjct 173295   CCAAGACTGTGTGGCGCAGGAGGCTGCCCGTGGACCGCATGTGGGAGGCCGGGACACCA 173354

Query 754      GCTTGGGCGCGTGGCGTGGCAAGTCAAGCTTGCTGTATGATGAGACACACTCTGTGGGG 813
Sbjct 173355   GCTTGGGCGCGTGGCGTGGCAAGTCAAGCTTGCTGTATGATGAGACACACTCTGTGGGG 173414

Query 814      GATCCCTGCTCTCCGAGGACTGGGTGCTGACAGCGCCCACTGCTCTCCCGAG 866
Sbjct 173415   GATCCCTGCTCTCCGAGGACTGGGTGCTGACAGCGCCCACTGCTCTCCCGAG 173467

```

Score = 289 bits (156), Expect = 4e-74  
Identities = 156/156 (100%), Gaps = 0/156 (0%)  
Strand=Plus/Plus

```

Query 38       CAGGTGAGGCGAGCTGGCTTAGCAGGCCCCACGCCACCGCTCTGCTCTCAGGCGCGCG 97
Sbjct 154680   CAGGTGAGGCGAGCTGGCTTAGCAGGCCCCACGCCACCGCTCTGCTCTCAGGCGCGCG 154739

Query 98       CTGCTGCGGGGCGCACCATGCTCTGCCCCAGGCGTGGAGACTGACCCGACCGCGCATAC 157
Sbjct 154740   CTGCTGCGGGGCGCACCATGCTCTGCCCCAGGCGTGGAGACTGACCCGACCGCGCATAC 154799

Query 158      CTCGAGGCTCCGCCCCCAGCTGCTGGACCCCCAGGCT 193
Sbjct 154800   CTCGAGGCTCCGCCCCCAGCTGCTGGACCCCCAGGCT 154835

```

Score = 268 bits (145), Expect = 5e-68  
Identities = 145/145 (100%), Gaps = 0/145 (0%)  
Strand=Plus/Plus

```

Query 1152     GCGCAACAGGCGCGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 1211
Sbjct 178425   GCGCAACAGGCGCGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 178484

Query 1212     AATGGCGCTGACTTCTATGAGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC 1271
Sbjct 178485   AATGGCGCTGACTTCTATGAGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCC 178544

Query 1272     GAGGGTGGCATTGATGCTCTGCCAGG 1296
Sbjct 178545   GAGGGTGGCATTGATGCTCTGCCAGG 178569

```

Score = 248 bits (134), Expect = 6e-62  
Identities = 134/134 (100%), Gaps = 0/134 (0%)  
Strand=Plus/Plus

```

Query 403      CAGTGCAGGTCAAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAGAGCGAAGGAGCGT 462
Sbjct 172624   CAGTGCAGGTCAAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAGAGCGAAGGAGCGT 172683

Query 463      GCGCGCTGCTGTGCTCTTCGAGCTCCAAAGCGCGGGTAGCCGAGCTCAGCTGCGAGAGA 522

```

Sbjct 172684 GGCGGCTGCTGTGCTCTCTCGCGCTCCAAACGCCAGGAGTACCGGACTCAGCTGCGAGGAGA 172743  
 Query 523 TGGGCTTCTCTCAGG 536  
 Sbjct 172744 TGGGCTTCTCTCAGG 172757

Score = 228 bits (123), Expect = 8e-56  
 Identities = 128/130 (98%), Gaps = 1/130 (0%)  
 Strand=Plus/Plus

Query 533 CAGGGCACTGACCCCACTCCGAGCTGGACGTGCGAACCGCGGGCGCCAAATGGCACGTGCGG 592  
 Sbjct 172825 CAGGGCACTGACCCCACTCCGAGCTGGACGTGCGAACCGCGGGCGCCAAATGGCACGTGCGG 172884  
 Query 593 CTCTCTCTGTGTGGAAGAGGGAGGCTGCCCAACACCGAGGGCTGTGAGAGTTCATCTC 652  
 Sbjct 172885 CTCTCTCTGTGTGGAAGAGGGAGGCTGCCCAACACCGAGGGCTGTGAGAGTTCATCTC 172944  
 Query 653 CGTGTG-TGA 661  
 Sbjct 172945 CGTGTGTGA 172954

Score = 191 bits (103), Expect = 1e-44  
 Identities = 103/103 (100%), Gaps = 0/103 (0%)  
 Strand=Plus/Plus

Query 261 GGTGGCCGGAATGTGSCCATCTGCTCTCCAGACCCAGGTGGAGCTCTCATCTCGCGGGAGCC 320  
 Sbjct 162138 GGTGGCCGGAATGTGSCCATCTGCTCTCCAGACCCAGGTGGAGCTCTCATCTCGCGGGAGCC 162197  
 Query 321 CTGCTACTTCTGACAGCCATCGGGGCGGCATCTCGGCCATTG 363  
 Sbjct 162198 CTGCTACTTCTGACAGCCATCGGGGCGGCATCTCGGCCATTG 162240

Score = 189 bits (102), Expect = 4e-44  
 Identities = 102/102 (100%), Gaps = 0/102 (0%)  
 Strand=Plus/Plus

Query 1052 CACAGAAATACATCCAGCCTGTGTGCTCCAGCTGCGCGCCAGGCGCTGTGGATGGCAA 1111  
 Sbjct 178132 CACAGAAATACATCCAGCCTGTGTGCTCCAGCTGCGCGCCAGGCGCTGTGGATGGCAA 178191  
 Query 1112 GATCTGTACCGTGAAGGGCTGGGCAACACGAGTACTATGG 1153  
 Sbjct 178192 GATCTGTACCGTGAAGGGCTGGGCAACACGAGTACTATGG 178233

Score = 137 bits (74), Expect = 1e-28  
 Identities = 74/74 (100%), Gaps = 0/74 (0%)  
 Strand=Plus/Plus

Query 191 GGTCCCAACCTTGGCCAGAGGTGAGCCAGGGAATCATTAACAGAGGCAGTGACATGGC 250  
 Sbjct 155413 GGTCCCAACCTTGGCCAGAGGTGAGCCAGGGAATCATTAACAGAGGCAGTGACATGGC 155472  
 Query 251 GCAGAAAGGAGGGTG 264  
 Sbjct 155473 GCAGAAAGGAGGGTG 155486

Score = 80.5 bits (43), Expect = 2e-11  
 Identities = 43/43 (100%), Gaps = 0/43 (0%)  
 Strand=Plus/Plus

Query 363 GTGGCTGTCTCTCTCAGAGGTGACCAAGGAGCCGCTGTATCCAG 405  
 Sbjct 162323 GTGGCTGTCTCTCTCAGAGGTGACCAAGGAGCCGCTGTATCCAG 162365

Score = 78.7 bits (42), Expect = 9e-11  
 Identities = 42/42 (100%), Gaps = 0/42 (0%)  
 Strand=Plus/Plus

Query 658 GTGATTGCCCAAGAGGCGGTTTCTTGCGCCCATCTGCGAAG 699  
 Sbjct 173082 GTGATTGCCCAAGAGGCGGTTTCTTGCGCCCATCTGCGAAG 173123

>dbj|AK091988.1| Homo sapiens cDNA FLJ34669 fis, clone LIVER2001051  
 Length=2547

Sort alignments for this subject sequence by:  
 E value Score Percent identity  
 Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165  
 Identities = 323/325 (99%), Gaps = 0/325 (0%)  
 Strand=Plus/Plus

Query 1459 AGACTCACTCCGAAGCCAGCGGACATGGTGACCCAGCTCTGACCGGTGCTTCTCGCTGCG 1518  
 Sbjct 2223 AGACTCACTCCGAAGCCAGCGGACATGGTGACCCAGCTCTGACCGGTGCTTCTCGCTGCG 2282  
 Query 1519 CAGCCTCCAGGAGCCGAGGTGATCCCGTGGTGGATCCAGCTGGGCGAGGATGGGAC 1578



```

Sbjct 2283 CAGCCTCCAGGGCCGAGGGTGTACCCGGTGTGGATCCACGCTGGGCCTAGGATGGAC 2342
Query 1579 GTTTTCTCTCTTGGGCCCCGGTCCACAGGTCCAGGACACCTCCCTCCAGGGTCTCTCT 1638
Sbjct 2343 GTTTTCTCTCTTGGGCCCCGGTCCACAGGTCCAGGACACCTCCCTCCAGGGTCTCTCT 2402
Query 1639 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCAACCTCTCTGACCCCAT 1698
Sbjct 2403 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCAACCTCTCTGACCCCAT 2462
Query 1699 GTAAATATTGTCTGCTGTCTGGGACTCTGTCTAGGTGCCCTGATGATGGATGCTCT 1758
Sbjct 2463 GTAAATATTGTCTGCTGTCTGGGACTCTGTCTAGGTGCCCTGATGATGGATGCTCT 2522
Query 1759 TTAAATAATAAAGATGGTTTGGATT 1783
Sbjct 2523 TTAAATAATAAAGATGGTTTGGATT 2547

```

Score = 315 bits (170), Expect = 6e-82  
Identities = 172/173 (99%), Gaps = 0/173 (0%)  
Strand=Plus/Plus

```

Query 1288 CCTGCCAGGGCCGACAGCGGTGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 1347
Sbjct 1836 CCTCCCAAGGGCCGACAGCGGTGTCCCTTTGTGTGTGAGGACAGCATCTCTCGGACGCCAC 1895
Query 1348 GTTGGCGGTGTGTGGCATGTGAGTGGGGCACTGGCTGTGCCCTGGCCAGGAAGCCAG 1407
Sbjct 1896 GTTGGCGGTGTGTGGCATGTGAGTGGGGCACTGGCTGTGCCCTGGCCAGGAAGCCAG 1955
Query 1408 GCGTCTACACAAAGTCAAGTGAATTCCTCGGAGTGGATCTTCAGGCCATAAAG 1460
Sbjct 1956 GCGTCTACACAAAGTCAAGTGAATTCCTCGGAGTGGATCTTCAGGCCATAAAG 2008

```

Score = 268 bits (145), Expect = 5e-68  
Identities = 145/145 (100%), Gaps = 0/145 (0%)  
Strand=Plus/Plus

```

Query 1152 GGCACACAGGCGGGGTACTCTCAGGAGGCTCGAGTCCCAATAATCAGCAATGATGTCTGC 1211
Sbjct 1514 GGCACACAGGCGGGGTACTCTCAGGAGGCTCGAGTCCCAATAATCAGCAATGATGTCTGC 1573
Query 1212 AATGGCGTGAATCTCTATGGAACAGATCAAGGCCAAGATGTTCTGTGCTGGCTACCCC 1271
Sbjct 1574 AATGGCGTGAATCTCTATGGAACAGATCAAGGCCAAGATGTTCTGTGCTGGCTACCCC 1633
Query 1272 GAGGGTGGCATTGATGCCCTGCCAGG 1296
Sbjct 1634 GAGGGTGGCATTGATGCCCTGCCAGG 1658

```

Score = 193 bits (104), Expect = 3e-45  
Identities = 104/104 (100%), Gaps = 0/104 (0%)  
Strand=Plus/Plus

```

Query 1050 CTCACAGATATACATCCAGCCTGTGTGCTCCAGACTGCGGCGAAGCCCTGTGGATGGC 1109
Sbjct 1219 CTCACAGATATACATCCAGCCTGTGTGCTCCAGACTGCGGCGAAGCCCTGTGGATGGC 1278
Query 1110 AAGATCTGTATCCGTGACGGGCTGGGGCAACAGCACTATATGG 1153
Sbjct 1279 AAGATCTGTATCCGTGACGGGCTGGGGCAACAGCACTATATGG 1322

```

>gb|AC020907.6| Homo sapiens chromosome 19 clone CTD-252T121, complete sequence  
Length=169891

Sort alignments for this subject sequence by:  
E value Score Percent identity  
Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165  
Identities = 323/325 (99%), Gaps = 0/325 (0%)  
Strand=Plus/Plus

```

Query 1459 AGACTCACTCCGAAAGCCAGCGGATGGTGACCCAGCTCTGACCGGTGGCTTCTGCTGCG 1518
Sbjct 79750 AGACTCACTCCGAAAGCCAGCGGATGGTGACCCAGCTCTGACCGGTGGCTTCTGCTGCG 79809
Query 1519 CAGCCTCCAGGGCCGAGGTGATCCCGTGGTGGGATCCACGCTGGGCGCAGGATGGGAC 1578
Sbjct 79810 CAGCCTCCAGGGCCGAGGTGATCCCGTGGTGGGATCCACGCTGGGCGCAGGATGGGAC 79869
Query 1579 GTTTTCTCTCTTGGGCCCCGGTCCACAGGTCCAGGACACCTCCCTCCAGGGTCTCTCTCT 1638
Sbjct 79870 GTTTTCTCTCTTGGGCCCCGGTCCACAGGTCCAGGACACCTCCCTCCAGGGTCTCTCTCT 79929
Query 1639 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCAACCTCTCTGACCCCAT 1698
Sbjct 79930 TCCACAGTGGCGGGCCCACTCAGCCCCGAGACACCCAACTCAACCTCTCTGACCCCAT 79989
Query 1699 GTAAATATTGTCTGCTGTCTGGGACTCTGTCTAGGTGCCCTGATGATGGATGCTCT 1758
Sbjct 79990 GTAAATATTGTCTGCTGTCTGGGACTCTGTCTAGGTGCCCTGATGATGGATGCTCT 80049

```

Query 1759 TTAAATAATAAGATGGTTTGGATT 1783  
 Sbjct 80050 TTAAATAATAAGATGGTTTGGATT 80074

Score = 353 bits (191), Expect = 1e-93  
 Identities = 199/202 (98%), Gaps = 3/202 (1%)  
 Strand=Plus/Plus

Query 858 TTCCC-GG-A-GGCGAACCAGGCTCTGTCCCGATGGCGAGTGTTTGCAGGTCCCGTGGCC 914  
 Sbjct 74119 TTCCCAGGTAGGCGGAAACCGGGTCTGTCCCGATGGCGAGTGTTTGCAGGTCCCGTGGCC 74178  
 Query 915 CAGGCTCTCCCCACGGCTCTGAGCTGGGGGTGCAAGCTGTGGTCTACCAACGGGGCTAT 974  
 Sbjct 74179 CAGGCTCTCCCCACGGCTCTGAGCTGGGGGTGCAAGCTGTGGTCTACCAACGGGGCTAT 74238  
 Query 975 CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGTGCTCAACTC 1034  
 Sbjct 74239 CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGTGCTCAACTC 74298  
 Query 1035 TCCAGTCCCCCTGCCCTTCACAG 1056  
 Sbjct 74299 TCCAGTCCCCCTGCCCTTCACAG 74320

Score = 315 bits (170), Expect = 6e-82  
 Identities = 172/173 (99%), Gaps = 0/173 (0%)  
 Strand=Plus/Plus

Query 1288 CCTGCCAGGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGAGCGCCAC 1347  
 Sbjct 79363 CCTCCACAGGCGACAGCGGTGGTCCCTTTGTGTGTGAGGACAGCATCTCTCGAGCGCCAC 79422  
 Query 1348 GTTGGCGGCTGTGTGGCATTTGTGAGTTGGGGCATCTGGCTGTGCTCCCTGGCCAGAGCCAG 1407  
 Sbjct 79423 GTTGGCGGCTGTGTGGCATTTGTGAGTTGGGGCATCTGGCTGTGCTCCCTGGCCAGAGCCAG 79482  
 Query 1408 GCGTCTACACCAAGTCAAGTACTTCCGGGAGTGGATCTTCCAGGCCATAAAG 1460  
 Sbjct 79483 GCGTCTACACCAAGTCAAGTACTTCCGGGAGTGGATCTTCCAGGCCATAAAG 79535

Score = 313 bits (169), Expect = 2e-81  
 Identities = 172/173 (99%), Gaps = 1/173 (0%)  
 Strand=Plus/Plus

Query 695 CCA-AGACTGTGGCGCGAGGAGCTGCCCGTGGACCGCATCGTGGAGGCGGGGACACCA 753  
 Sbjct 73844 CCAAGACTGTGGCGCGAGGAGCTGCCCGTGGACCGCATCGTGGAGGCGGGGACACCA 73903  
 Query 754 GCTTGGGCGGTGGCGGCTGGCAAGTCAGGCTTCGCTATGATGGAGCAACCTCTGTGGGG 813  
 Sbjct 73904 GCTTGGGCGGTGGCGGCTGGCAAGTCAGGCTTCGCTATGATGGAGCAACCTCTGTGGGG 73963  
 Query 814 GATCCCTGTCTCTCCGGGAGCTGGGTGTGAGACGCGCCCACTGCTTCCCGAG 866  
 Sbjct 73964 GATCCCTGTCTCTCCGGGAGCTGGGTGTGAGACGCGCCCACTGCTTCCCGAG 74016

Score = 289 bits (156), Expect = 4e-74  
 Identities = 156/156 (100%), Gaps = 0/156 (0%)  
 Strand=Plus/Plus

Query 38 CAGGTGAGGCGAGCTGGCTAGCAGGGCCCCACGCCACCGGCTCTGCTCCAGGCGCCCG 97  
 Sbjct 55222 CAGGTGAGGCGAGCTGGCTAGCAGGGCCCCACGCCACCGGCTCTGCTCCAGGCGCCCG 55281  
 Query 98 CTGCTGGCGGGCCACCATGCTCTCTGCCAGCGCTGGAGACTGAACCGAGCCCGGCACTAC 157  
 Sbjct 55282 CTGCTGGCGGGCCACCATGCTCTCTGCCAGCGCTGGAGACTGAACCGAGCCCGGCACTAC 55341  
 Query 158 CTCGAGGCTTCGCCCCCACTGCTGGAGCCCAAGGTT 193  
 Sbjct 55342 CTCGAGGCTTCGCCCCCACTGCTGGAGCCCAAGGTT 55377

Score = 268 bits (145), Expect = 5e-68  
 Identities = 145/145 (100%), Gaps = 0/145 (0%)  
 Strand=Plus/Plus

Query 1152 GGCCCAACAGGCGCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 1211  
 Sbjct 79041 GGCCCAACAGGCGCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 79100  
 Query 1212 AATGGCGCTGACTTCTATGGAAACAGATCAAGCCCCAAGATGTTCTGTGCTGGCTACCCC 1271  
 Sbjct 79101 AATGGCGCTGACTTCTATGGAAACAGATCAAGCCCCAAGATGTTCTGTGCTGGCTACCCC 79160  
 Query 1272 GAGGGTGGCATTGATGCTGCTGCGAG 1296  
 Sbjct 79161 GAGGGTGGCATTGATGCTGCTGCGAG 79185

Score = 248 bits (134), Expect = 6e-62  
 Identities = 134/134 (100%), Gaps = 0/134 (0%)  
 Strand=Plus/Plus

Query 403 CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTTGAACAAGACGGAAAGGACGT 462  
 Sbjct 73173 CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTTGAACAAGACGGAAAGGACGT 73232

Query 463 GCGCGCTGCTGTGCTCTCGCGCTCCACGCCACGGGTAGCCGGACTCAGCTGCGAGGAGA 522  
 Sbjct 73233 GCGCGCTGCTGTGCTCTCGCGCTCCACGCCACGGGTAGCCGGACTCAGCTGCGAGGAGA 73292

Query 523 TGGGCTTCTCTCAGG 536  
 Sbjct 73293 TGGGCTTCTCTCAGG 73306

Score = 233 bits (126), Expect = 2e-57  
 Identities = 129/130 (99%), Gaps = 1/130 (0%)  
 Strand=Plus/Plus

Query 533 CAGGGCACTGACCCACTCCGAGCTGGACGTGCAACGGCGGGCCCAATGGCAAGTCTGGG 592  
 Sbjct 73374 CAGGGCACTGACCCACTCCGAGCTGGACGTGCAACGGCGGGCCCAATGGCAAGTCTGGG 73433

Query 593 CTCTCTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGAGAGGTATCTC 652  
 Sbjct 73434 CTCTCTCTGTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGAGAGGTATCTC 73493

Query 653 CGTGTG-TGA 661  
 Sbjct 73494 CGTGTGTGA 73503

Score = 193 bits (104), Expect = 3e-45  
 Identities = 104/104 (100%), Gaps = 0/104 (0%)  
 Strand=Plus/Plus

Query 1050 CTACAGAAATACATCCAGCTCTGTGTGCTTCCAGCTGCGCGGACAGGCCCTGGTGGATGGC 1109  
 Sbjct 78746 CTACAGAAATACATCCAGCTCTGTGTGCTTCCAGCTGCGCGGACAGGCCCTGGTGGATGGC 78805

Query 1110 AAGATCTGTACCGTGAACGGCTGGGGCAACACGAGTACTATGG 1153  
 Sbjct 78806 AAGATCTGTACCGTGAACGGCTGGGGCAACACGAGTACTATGG 78849

Score = 191 bits (103), Expect = 1e-44  
 Identities = 103/103 (100%), Gaps = 0/103 (0%)  
 Strand=Plus/Plus

Query 261 GGTGGCCGGAATCTGSCCATGCTGCTCCAGACCCAGGTGGCAGCTCTCACTGCGGGGACC 320  
 Sbjct 62792 GGTGGCCGGAATCTGSCCATGCTGCTCCAGACCCAGGTGGCAGCTCTCACTGCGGGGACC 62851

Query 321 CTGCTACTTCTGACAGCCATCGGGGCGGCATCTGGGCCATTG 363  
 Sbjct 62852 CTGCTACTTCTGACAGCCATCGGGGCGGCATCTGGGCCATTG 62894

Score = 137 bits (74), Expect = 1e-28  
 Identities = 74/74 (100%), Gaps = 0/74 (0%)  
 Strand=Plus/Plus

Query 191 GGTCCCAACCTGGCCCAAGAGGTTCAGCCAGGGAATCATTAAACAAGAGGCAATGACATGGC 250  
 Sbjct 55955 GGTCCCAACCTGGCCCAAGAGGTTCAGCCAGGGAATCATTAAACAAGAGGCAATGACATGGC 56014

Query 251 GCAGAGGAGAGGGTG 264  
 Sbjct 56015 GCAGAGGAGAGGGTG 56028

Score = 82.4 bits (44), Expect = 7e-12  
 Identities = 44/44 (100%), Gaps = 0/44 (0%)  
 Strand=Plus/Plus

Query 1 TCGAGCCCGCTTTCCAGGACCCCTACCTGAGGGGCCACAGGTGA 44  
 Sbjct 54009 TCGAGCCCGCTTTCCAGGACCCCTACCTGAGGGGCCACAGGTGA 54052

Score = 80.5 bits (43), Expect = 2e-11  
 Identities = 43/43 (100%), Gaps = 0/43 (0%)  
 Strand=Plus/Plus

Query 363 GTGGCTGTCTCTCTCAGGAGTGACCAAGGACCGCTGTATCCAG 405  
 Sbjct 62977 GTGGCTGTCTCTCTCAGGAGTGACCAAGGACCGCTGTATCCAG 63019

Score = 78.7 bits (42), Expect = 9e-11  
 Identities = 42/42 (100%), Gaps = 0/42 (0%)  
 Strand=Plus/Plus

Query 658 GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAG 699  
 Sbjct 73631 GTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAG 73672

>dbj|AK125670.1| Homo sapiens cDNA FLJ43662 fis, clone TBARS2001258, weakly similar to SERINE PROTEASE HEPsin (EC 3.4.21.-)  
Length=2631

Sort alignments for this subject sequence by:  
E value    Score    Percent identity  
Query start position    Subject start position

Score = 353 bits (191), Expect = 1e-93  
Identities = 199/202 (99%), Gaps = 3/202 (1%)  
Strand=Plus/Plus

Query	858	TTCCCTCG-A-GCGGAAACCGGCTCTGTCCTCCGATGGCAGTGTGTCCTGGCTGCTGCTGCTG	914
Sbjct	1437	TTCCCTCGTATGGCGGAAACCGGCTCTGTCCTCCGATGGCAGTGTGTCCTGGCTGCTGCTGCTG	1496
Query	915	CAGGCTCTCTCCCAACGCTCTGCACTGGGGGTGCAGGCTGTGGTCTACCAAGGGGCTAT	974
Sbjct	1497	CAGGCTCTCTCCCAACGCTCTGCACTGGGGGTGCAGGCTGTGGTCTACCAAGGGGCTAT	1556
Query	975	CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTC	1034
Sbjct	1557	CTTCCCTTTTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTGCCCTGGTCCACCTC	1616
Query	1035	TCCAGTCCCCCTGCCCTCAAG	1056
Sbjct	1617	TCCAGTCCCCCTGCCCTCAAG	1638

Score = 313 bits (169), Expect = 2e-81  
Identities = 172/173 (99%), Gaps = 1/173 (0%)  
Strand=Plus/Plus

Query	695	CCA-AGACTGTGGCCACAGAAAGCTGCCCTGGACCGCATCTGTGGAGGCGGAGACCA	753
Sbjct	1162	CCACAGACTGTGGCCACAGAAAGCTGCCCTGGACCGCATCTGTGGAGGCGGAGACCA	1221
Query	754	GCTTGGGCGCGTGGCCGTGGCAAGTCAAGCTCTTCGTATGATGAGACCACTCTGTGGG	813
Sbjct	1222	GCTTGGGCGCGTGGCCGTGGCAAGTCAAGCTCTTCGTATGATGAGACCACTCTGTGGG	1281
Query	814	GATCCCTGCTCTCCGAGGAGCTGGGTGTGACAGCGCCCACTGCTTCCCGAG	866
Sbjct	1282	GATCCCTGCTCTCCGAGGAGCTGGGTGTGACAGCGCCCACTGCTTCCCGAG	1334

Score = 248 bits (134), Expect = 6e-62  
Identities = 134/134 (100%), Gaps = 0/134 (0%)  
Strand=Plus/Plus

Query	403	CAGTCAAGGTCAAGCTCTGCGAGCTCGGCTCATGGTCTTTGACAGAGACGAGAGGAGCT	462
Sbjct	490	CAGTCAAGGTCAAGCTCTGCGAGCTCGGCTCATGGTCTTTGACAGAGACGAGAGGAGCT	549
Query	463	GGCGGCTGTGTGCTCTCTCGCGCTCCAAACGCGAGGATAGCGGAGCTCAGCTGCGAGGAG	522
Sbjct	550	GGCGGCTGTGTGCTCTCTCGCGCTCCAAACGCGAGGATAGCGGAGCTCAGCTGCGAGGAG	609
Query	523	TGGGCTTCTCTCAGG	536
Sbjct	610	TGGGCTTCTCTCAGG	623

Score = 233 bits (126), Expect = 2e-57  
Identities = 129/130 (99%), Gaps = 1/130 (0%)  
Strand=Plus/Plus

Query	533	CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAAACGGCGGGCGCCAAAGCAGCTCGG	592
Sbjct	591	CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAAACGGCGGGCGCCAAAGCAGCTCGG	750
Query	593	CTTCTTTCTGTGTGAGCAAGGGGAGGCTGCCGCCACACCCAGAGGCTGCTGAGAGTCATCTC	652
Sbjct	752	CTTCTTTCTGTGTGAGCAAGGGGAGGCTGCCGCCACACCCAGAGGCTGCTGAGAGTCATCTC	810
Query	653	CGTGTG-TGA	661
Sbjct	811	CGTGTGTGA	820

Score = 78.7 bits (42), Expect = 9e-11  
Identities = 42/42 (100%), Gaps = 0/42 (0%)  
Strand=Plus/Plus

Query	658	GTGATTGCCCCAGAGGGCCGTTCTTGGCCGCCATCTGCCAAG	699
Sbjct	948	GTGATTGCCCCAGAGGGCCGTTCTTGGCCGCCATCTGCCAAG	989

>gb|DQ677665.1| Homo sapiens sodium channel beta-1 subunit precursor (SCN1B)  
gene, complete cds  
Length=15819

Sort alignments for this subject sequence by:  
E value    Score    Percent identity  
Query start position    Subject start position

Score = 289 bits (156), Expect = 4e-74  
 Identities = 156/156 (100%), Gaps = 0/156 (0%)  
 Strand=Plus/Plus

```

Query 38      CAGGTTGAGGCAGCCTGGCCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCG 97
Sbjct 14090   CAGGTTGAGGCAGCCTGGCCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCG 14149
Query 98      CTGCTGCGGGGCCACCATGCTCCTGCCCCAGGCTGGAGACTGACCCGACCCCGCACTAC 157
Sbjct 14150   CTGCTGCGGGGCCACCATGCTCCTGCCCCAGGCTGGAGACTGACCCGACCCCGCACTAC 14209
Query 158     CTGAGGCTTCGCCCCCACTGCTGGAACCCAGGGT 193
Sbjct 14210   CTCAGGCTTCGCCCCCACTGCTGGAACCCAGGGT 14245

```

Score = 137 bits (74), Expect = 1e-28  
 Identities = 74/74 (100%), Gaps = 0/74 (0%)  
 Strand=Plus/Plus

```

Query 191     GGTCCCAACCTTGGCCCAAGAGGTCAGCCAGGGAAATCAITTAACAAGAGGCAGTGAATGGC 250
Sbjct 14823   GGTCCCAACCTTGGCCCAAGAGGTCAGCCAGGGAAATCAITTAACAAGAGGCAGTGAATGGC 14882
Query 251     GCAGAAAGAGGGTG 264
Sbjct 14883   GCAGAAAGAGGGTG 14896

```

Score = 82.4 bits (44), Expect = 7e-12  
 Identities = 44/44 (100%), Gaps = 0/44 (0%)  
 Strand=Plus/Plus

```

Query 1       TCAGGCCCGCTTTCCAGGACCTACCTGAGGGCCCAAGGTGA 44
Sbjct 12877   TCAGGCCCGCTTTCCAGGACCTACCTGAGGGCCCAAGGTGA 12920

```

>gb|AC197610.3| MACACA MULATTA BAC clone CH250-34898 from chromosome 19, complete  
 sequence  
 Length=158733

Sort alignments for this subject sequence by:  
 E value    Score    Percent identity  
 Query start position    Subject start position

Score = 250 bits (135), Expect = 2e-62  
 Identities = 149/156 (95%), Gaps = 0/156 (0%)  
 Strand=Plus/Plus

```

Query 38      CAGGTTGAGGCAGCCTGGCCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCG 97
Sbjct 149463   CAGGTTGAGGCAGCCTGGCCCTAGCAGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCG 149522
Query 98      CTGCTGCGGGGCCACCATGCTCCTGCCCCAGGCTGGAGACTGACCCGACCCCGCACTAC 157
Sbjct 149523   CTGCTGCGGGGCCACCATGCTCCTGCCCCAGGCTGGAGACTGACCCGACCCCGCACTAC 149582
Query 158     CTCGAGGCTTCGCCCCCACTGCTGGAACCCAGGGT 193
Sbjct 149583   CTCGAGGCTTCGCCCCCACTGCTGGAACCCAGGGT 149618

```

Score = 180 bits (97), Expect = 2e-41  
 Identities = 101/103 (98%), Gaps = 0/103 (0%)  
 Strand=Plus/Plus

```

Query 261     GGTGGCCGGAAGTGTGCAATGCTGTCCAGAACCGAGTGGCAGCTCTCACTGCGGGGACC 320
Sbjct 157187   GGTGGCCGGAAGTGTGCAATGCTGTCCAGAACCGAGTGGCAGCTCTCACTGCGGGGACC 157246
Query 321     CTGCTACTTCTGACAGCCATCGGGGCGGCATCTCGGGCAATG 363
Sbjct 157247   CTGCTACTTCTGACAGCCATCGGGGCGGCATCTCGGGCAATG 157289

```

Score = 132 bits (71), Expect = 6e-27  
 Identities = 73/74 (98%), Gaps = 0/74 (0%)  
 Strand=Plus/Plus

```

Query 191     GGTCCCAACCTTGGCCCAAGAGGTCAGCCAGGGAAATCAITTAACAAGAGGCAGTGAATGGC 250
Sbjct 150194   GGTCCCAACCTTGGCCCAAGAGGTCAGCCAGGGAAATCAITTAACAAGAGGCAGTGAATGGC 150253
Query 251     GCAGAAAGAGGGTG 264
Sbjct 150254   GCAGAAAGAGGGTG 150267


```

Score = 75.0 bits (40), Expect = 1e-09  
 Identities = 42/43 (97%), Gaps = 0/43 (0%)  
 Strand=Plus/Plus

```

Query 363     GTGGCTGTCTCTCTCAGAGGTGACCAAGGAGCGCTGTATCCAG 405
Sbjct 157372   GTGGCTGTCTCTCTCAGAGGTGACCAAGGAGCGCTGTATCCAG 157414

```


>ref|XM\_001719305.1|  PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA  
Length=1287

Score = 207 bits (112), Expect = 1e-49  
Identities = 112/112 (100%), Gaps = 0/112 (0%)  
Strand=Plus/Minus

```

Query 403  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAAGGACGT 462
Sbjct 513  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAAGGACGT 454
Query 463  GGCAGCTGCTGTGCTCCTCGCGCTCCAAAGCCAGGGTAGCCGACTCAGCTG 514
Sbjct 453  GGCAGCTGCTGTGCTCCTCGCGCTCCAAAGCCAGGGTAGCCGACTCAGCTG 402

```


>ref|XM\_001721961.1|  PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA  
Length=1287

Score = 207 bits (112), Expect = 1e-49  
Identities = 112/112 (100%), Gaps = 0/112 (0%)  
Strand=Plus/Minus

```

Query 403  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAAGGACGT 462
Sbjct 513  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAAGGACGT 454
Query 463  GGCAGCTGCTGTGCTCCTCGCGCTCCAAAGCCAGGGTAGCCGACTCAGCTG 514
Sbjct 453  GGCAGCTGCTGTGCTCCTCGCGCTCCAAAGCCAGGGTAGCCGACTCAGCTG 402

```


>ref|XM\_001719287.1|  PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA  
Length=1287

Score = 207 bits (112), Expect = 1e-49  
Identities = 112/112 (100%), Gaps = 0/112 (0%)  
Strand=Plus/Minus

```

Query 403  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAAGGACGT 462
Sbjct 513  CAGTGCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAAGGACGT 454
Query 463  GGCAGCTGCTGTGCTCCTCGCGCTCCAAAGCCAGGGTAGCCGACTCAGCTG 514
Sbjct 453  GGCAGCTGCTGTGCTCCTCGCGCTCCAAAGCCAGGGTAGCCGACTCAGCTG 402

```

>gb|AC158993.2|  Mus musculus BAC clone RP24-427N13 from chromosome 7, complete sequence  
Length=179746

Sort alignments for this subject sequence by:  
E value Score Percent identity  
Query start position Subject start position

Score = 141 bits (76), Expect = 1e-29  
Identities = 122/145 (84%), Gaps = 0/145 (0%)  
Strand=Plus/Minus

```

Query 1152  GGCCACACAGGCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 1211
Sbjct 61803  GGCCACACAGGCTATGGTCTCCAGAGGCGGGGTTCCTCATAGCAACAGAGATTTC 61744
Query 1212  AATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGCTACCC 1271
Sbjct 61743  AACAGCCCGACTTCTACAGGATCGATCAAGCCCAAGATGTTCTGTGCTGCTATCT 61684
Query 1272  GAGGGTGGCATTGATGCTGCCAGG 1296
Sbjct 61683  GAGGGTGGCATTGATGCTGCCAGG 61659

```

Score = 119 bits (64), Expect = 5e-23  
Identities = 92/105 (87%), Gaps = 4/105 (3%)  
Strand=Plus/Minus

```

Query 261  GGTGGCCGACTG-TGCCATGCTGCTCCAGACCCAGGTGGCAGCTCTCACTGCGGGGAC 319
Sbjct 71347  GGTGGCCGACTGCAG-CATGCTGCTCCAGACCCAGGTGGCAGCTCTCACTTGTGGTAC 71289
Query 320  CTTGCTACTTC-TGACAGCCATCGGGGCGCATCCTCGGCGCAATTG 363
Sbjct 71288  CTTGCTG-TTCCTGACAGGCATCGGGGCGCGCTCTGGGCAATTG 71245

```

Database: All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: May 19, 2008 5:44 PM

Number of letters in database: 2,000,849,822

Number of sequences in database: 6,839,787

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 6839787

Number of Hits to DB: 3671278

Number of extensions: 17

Number of successful extensions: 17

Number of sequences better than 10: 3

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 16

Number of HSP's successfully gapped: 16

Length of query: 1783

Length of database: 23768953950

Length adjustment: 33

Effective length of query: 1750

Effective length of database: 23543240979

Effective search space: 41200671713250

Effective search space used: 41200671713250

A: 0

X1: 15 (28.8 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 15 (28.8 bits)

S2: 23 (43.6 bits)